SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: Innogenetics sa.
 - (B) STREET: Industriepark Zwijnaarde 7, box 4
 - (C) CITY: Gheat
 - (E) COUNTRY: Belgium
 - (F) POSTAL CODE (ZIP): B-9052
 - (G) TELEPHONE: 00 32 9 241 07 11
 - (H) TELEFAX: 00 32 9 241 07 99
- (ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.
- (111) NUMBER OF SEQUENCES: 270
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (111) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR34-4-20
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
- CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly

 1 5 10 15
- GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

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AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 144

96

40

AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT 192 Arg Ala Ala Gly Leu Arg Ash Pro Asp Phe Leu Val Cys Gly Asp Asp

CTG GTC GTG GTG GCT GAG AGT 213 Leu Val Val Val Ala Glu Ser 65

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Ash Ser Lys Gly 10

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 40

Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp

Leu Val Val Val Ala Glu Ser 63

(2) INFORMATION FOR SEQ ID NO: 3:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(Vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-18

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:																
CTC	ACG	GAA	CGG	C::	TAC	TGC	GGG	GGC	CCI	ATG	TTC	AAC	AGC	AAG	GGG	48
Leu	Thr	Glu	AT3	Leu	1/=	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
ī				5					10					15		
GCC	CAG	TGT	GGT	TAT	CGC	CGC	TGC	CGI	GCC	AGT	GGA	GII	CIG	cci	ACC	96
Ala	Gln	Cys	Gly	:v:	وتد	Arg	Cys	Azq	Ala	Ser	Gly	Val	Leu	Pro	Thr	
•		•	20	•	_	Ī	-	25			•		30			
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGC	TAC	ATC	AAG	GCC	ACA	GCG	GCT	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	The	Cys	Tyr	Ile	Lys	Ala	The	Ala	Ala	Ala	
•	*	35		*			40	•		•		45				
AGG	GCC	GCX	GGC	CTC	CGG	AAC	CCG	GAC	TTT	CII	GTC	TGC	GGA	GAT	GAT	192
Arg	Ala	Ala	Gly	Leu	Arg	λsπ	Sio.	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
	50		·		-	55					60	-	•	•		-
CTG	GTC	GTG	GTG	GCT	GAG	AGT										213

(2) INFORMATION FOR SEQ ID NC: 4:

CTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 40

Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
50 55 60

Leu Val Val Val Ala Glu Ser

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (3) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear

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98	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(vii) IMMEDIATE SOURCE: (S) CLONE: BR36-23-18	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1213	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAG GGG Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly 1 5 10	. 48
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30	96
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA Ser Phe Gly Asn Thr lie Thr Cys Tyr IIe Lys Ala Thr Ala Ala Ala 35	144
AAA GCC GCA GGC CTC CGG AGC CCG GAC TIT CTT GTC TGC GGA GAT GAT Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60 CTG GTC GTG GTG GCT GAG AGT	192
Leu Val Val Val Ala Glu Ser 65 70	213
(2) INFORMATION FOR SEQ ID NO: 6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid	
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 725 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35

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Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60.

Leu Val Val Val Ala Glu Ser 65 70

- (2) INFORMATION FOR SEQ ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR36-23-20
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LCCATION: 1..213
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC ACG G	NG CGG CTT TAC TO	C GGG GGC CCT ATG T	PTT AAC AGC AAA GG:	43
Leu Thr Gl	lu Arg Leu Tyr Cy	s Gly Gly Pro Met P	he Asn Ser Lys Gly	,
1	5	10	15	

GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30

AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA 144
Ser Phe Gly Asn Thr lie Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala

AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
50
55
60

CTG GTC GTG GCT GAG AGT
Leu Val Val Ala Glu Ser
65 70

- (2) INFORMATION FOR SEQ ID NO: 8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii)	MOLECULE	TYPE.	protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10 15

Ala Gla Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

Ser Phe Gly Asm Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60

Leu Val Val Val Ala Glu Ser 65 70

(2) INFORMATION FOR SEQ ID NC: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CONA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (3) CLONE: BR33-2-17
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTC	ACG	GAG	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTC	AAC	AGC	AAG	GGG	48	
Leu '	Thr	Glu	Arg	Leu	Tyr	Суз	Gly	G1y	520	Met	Phe	Asn	Ser	Lvs	Glv	10	
1				5			•	•	10					15	,		

GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30

AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA

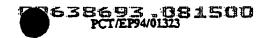
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala

35

40

45

AAA GCC GCA GGC CTC CGG AAC CCG GAC TIT CTT GTT TGC GGA GAT GAT 192



Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp so 55 60

TTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser 65 70 213

- (2) INFORMATION FOR SEQ ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTE: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 10 15

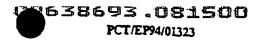
Ala Glm Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60

Leu Val Val Val Ala Glu Ser 65 70

- (2) INFORMATION FOR SEQ ID NO: 11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR33-2-21
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:



CTC ACG Leu Thr 1	GAG CGG Glu Arg	CTT TAC Leu Tyr 5	TGC GGG Cys Gly	GGC CCT Gly Pro	Met Phe	AAC AGC Ast Ser	TAR GIÀ	48
014	20	the wed	YLE CAR	Arg Ala	Ser Gly	GTT CTG Val Leu	Pro Thr	
AGT TTC Ser Phe	GGC AAC Gly Asn 35	ACA ATC Thr Ile	ACT TGT Thr Cys 40	Tyr Ile	AAG GCC Lys Ala	ACA GCG Thr Ala 45	GCT GCA Ala Ala	144
AAA GCC Lys Ala 50	GCA GGC Ala Gly	CTC CGG Leu Arg	AAC CCG Asn Pro 55	GAC TIT Asp Phe	CTT GTT Leu Val 60	TGC GGA Cys Gly	der der	192
TTG GTC (Leu Val (65	GTG GTG Val Val	GCT GAG Ala Glu 70	AGT Ser					213

- (2) INFORMATION FOR SEQ ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (a) TYPE: amine acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10

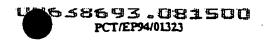
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60

Leu Val Val Val Ala Glu Ser

- (2) INFORMATION FOR SEQ ID NO: 13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-5

(ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

(XI) SEQUENCE DESCRIPTION. SEQ 15 No. 15.	
C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 1 5 10 15	46
GTG AGG GCC CTT GAA GAC GGG ATA AAT TIC GCA ACA GGG AAT TIG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro 20 25 30	94
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile 35	142
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val 50 55 60	190
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyt Glu Ala Asp Asp 65 70 75	238
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gla Asp Gly Asa 80 85 90 95	296
ACA TOT GOG TGC TGG ACC CCA GTG ACA COT ACA GTG GCA GTC AGG TAC Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr 100 105 110	334
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val 115 120 125	382
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526

GGA CAC CGA ATG GCT Gly His Arg Met Ala 180

541

- (2) INFORMATION FOR SEQ ID NO: 14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MCLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
- Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
- Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25 30
- Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
- Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
- Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90
- Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
- Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Mer Leu Val Gly
- Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 135 140
- Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 155 156
- Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly 165 170 175

His Arg Met Ala

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii)	MOL	CULE	TYF	PE: 0	ena										
(.ii)	HYPO	THE	CICAL	. NO											
(;	.ii)	ANT	-ser	isz :	NO											
(1	rii)		EDIA:				14									
I	(1x)	(A	TURE: NAM LOC	Æ/K			11									·
	(xi)	SEQ	UENC:	E DE	SCRI	PTIO	7: S	eg I	d no	: 15	:					
	C GG 1 G1 1	c GC	a Pr	o Va	A GG 1 Gl 5	A GGG y Gl;	C GT Y Va	C GC	A AG a Ar 1	g Al	C CT a Le	T GCC	G CA a Hi	T GG s Gl	Y	- 46
GTG :	AGG ATG	GCC Ala	CTT (Leu	GAA Glu 20	GAC Asp	GGG (ATA Ile	AAT Asn	TTC Phe 25	GCA Ala	ACA Thr	GGG :	AAT Asn	TTG Leu 30	510 CCC	94
GGT Gly	Cys TGC	TCC Ser	TTT Phe 35	TCT Ser	ATC Ile	TTC Phe	CTT	CCT Pro 40	GCT Ala	CTG Leu	TTC Phe	TCT Ser	TGC Cys 45	TTA Leu	ATC Ile	142
CAT His	CCA Pro	GCA Ala 50	GCT Ala	AGT Ser	CTA Leu	GAG Glu	TGG Trp 55	CGG Arg	AAC Asn	ACG Thr	TCT Ser	GGC Gly 60	CTC Leu	TAT Tyr	GTC Val	190
CTT Leu	ACC Thr 65	AAC	GAC Asp	TGT Cys	TCC Ser	አአፒ አsn 70	AGC Ser	AGT Ser	ATT Ile	GTG Val	TAT Tyr 75	GAG Glu	GCC Ala	GAT ÇEK	GAC Asp	239
Val	277	CTG Leu	CAC His	ACA Thr	CCC Pro	GGC GLY	TGT Cys	GTA Val	CCT Pro	TGT Cys	GTT Val	CAG Gln	GAC Asp	GGT Gly	AAT Asn 95	286
80 ACA Thr	TCT Ser	GCG Ala	TGC Cys	TGG Trp 100	ACC	CCA Pro	GTG Val	ACA Thr	CCT Pro 105	ACA Thr	GTG Val	GCA Ala	GTC Val	AGG Arg 110	LÀT	334
GTC Val	GGA Gly	GCA Ala	ACC Thr 115	acc Thr	GCT Ala	TCG Ser	ATA Ile	CGC Arg 120	Arg	CAT His	GTA Val	GAC Asp	ATA Ile 125	Leu	GTG Val	382
GGC Gly	GCG Ala	GCC Ala	Thr	ATG Met	TGC Cys	TCT Ser	GCT Ala	Leu	TAC Tyr	GTG Val	GGT	GAT Asp	Met	TGT Cys	GGG	430
GCC Ala	GTC Val	·	י רידר	GTG Val	GGA Gly	CAA Glm	GCC	TTC Phe	ACC The	TTC Phe	AGX	Pro	CG:	CGC	CAT His	479

SUBSTITUTE SHEET (RULE 26)

CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA

Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170

GGA CAC CGA ATG GCT Gly His Arg Mer Ala

541

- (2) INFORMATION FOR SEQ ID NO: 16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MCLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
- Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
- Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25
- Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His
- Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
- Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
- Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asm Thr
- Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
- Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
 115 120 125
- Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140
- Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 150 155 160
- Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 155 170 175

His Arg Met Ala 190

- (2) INFORMATION FOR SEQ ID NO: 17:
 - (i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH: 541 base pairs
(3)	TYPE: nucleic acid
(C)	STRANDEDNESS: single
(D)	TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(iii) HYPCTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE: (B) CLONE: HD10-2-21

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

	(XI)	25	(OEAN)	.2 01	.scx.		M: 2	, <u></u>	טא כ.	/: <u>1</u> ,	•					
	TC GC															46
Ve	al Gl 1	LY A	ia Pi	o va	5	ıy G:	. y vc	L' AL		.0	.d _e	iu mi	.a =1		. y . 5	
																•
	AGG Azq															94
V d.	æg	ALG	Leu	20	ASD	Gry	110	ASII	25	WTG	Las	917	A5	30	820	
				_												
	TGC															142
Gly	Cåa	Ser	Phe 35	Ser	Iie	Phe	Leu	Le:	Ala	Fen	Phe	Ser	C78	Leu	Ile	
			33					40					43			
CAT	CCA	GCλ	GCT	AGT	CTA	GAG	TGG	CGG	AAC	ACG	TCT	GGC	CEC	TAC	GTC	190
His	520		λla	Ser	Leu	Glu		Arg	Asn	Thr	Ser		Leu	Tyr	Val	
		50					55			•		60				
CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	GAC	238
Leu	The	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Giu	λla	Asp	Asp	
	65					70					75					
GTT	277	CTG	CAC	ACA	ccc	GGC	TGT	GTA	CCT	TGT	GTT	CAG	GAC	GGT	AAT	286
	Ile															
80					85					90					95	
3.73	ምረጥ	ece	TGC	TCC	3.00	CC3	CTC	AC2	CCT	202	GTG.	GCS	GTC	AGG	TAC	334
	Ser															55.
			•	100					105					110	•	
														***	CTC	382
															GTG Val	302
Val	GLY	VI	115	* ***	774	001		120	9	*****	14_	AUP	125			
								-								
															GGG	
GIÀ	WIS	130		met	cys	241	135	red	ryr	val	GTĀ	140	1155	Cys	Gly	

GCC Ala	GTC Val 145	TTC Phe	CTC Leu	GTG Val	GGA Gly	CAA Gln 150	Ala	TTC Phe	ACG Thr	TTC	AGA Arg 155	Br CCI	CGT	Arg CGC	CAT His	478
CAA Gln 160	ACG Thr	GTC Val	CAG Gln	ACC Thr	TGT Cys 165	AAC Asn	TGC Cys	TCA Ser	CTG Leu	TAC Tyr 170	CCY	GGC Gly	CAT His	CTT Leu	TCA Ser 175	526
			ATG Met													541

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MCLECULE TYPE: procein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Giu Ala Asp Asp Val 65 70 75 80

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val

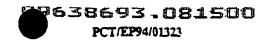
Gly Ala Thr Thr Ala Ser Ile Arg Arg Eis Val Asp Ile Leu Val Gly
115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
165 170 175

His Arg Met Ala



(2) INFORMATION FOR SEQ ID NO: 19:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 541 base pairs (B) TYPE: nucleic acid (C) STRANTEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NC	
(iii) ANTI-SENSE: NO	
(vii) IMMEDIATE SOURCE: (B) CLONE: BR36-9-13	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2541	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 1 5 10	46
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro 20 25 30	94
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	142

CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val
50 55 60

CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp
65 70 75

GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT

Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn

80 85 90 95

ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC

Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr

100 105 110

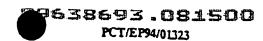
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG

Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val

115

120

125



GGC	GCG Ala	GCC Ala 130	* ***	ATG Met	TGC	TCA Ser	GCG Ala 135	CTC	TAC	GTG Val	GGT Gly	GAT Asp 140	ATG Met	TGT Cys	GGG	430
GCC Ala	GTC Val 145	TTC Phe	CTT	GTG Val	GGA Gly	CAA Gln 150	GCC Ala	TIC Phe	ACG Thr	TTC Phe	AGA Arg 155	CCT Pro	CGT Arg	CGC Arg	CAT His	478
CAA Gin 160	ACG Thr	GTC Val	CAG Gin	ACC Thr	TGT Cys 163	aac asn	TGC Cys	TCG Ser	CTG Leu	TAC Tyr 170	CCA Pro	GGC Gly	CAT His	CTT Leu	TCA Ser 175	525
GGA Gly																541

(2) INFORMATION FOR SEQ ID NO: 20:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amine acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20: Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
65 70 75 80

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 160

Thr Val Gln Thr Cys Asm Cys Ser Leu Tyr Pro Gly His Leu Ser Gly

111 ^{*}

PCT/EP94/01323

165 170 175

His	Arg	Mec	Ala
			190

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR36-9-20
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

100

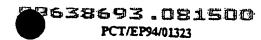
- (B) LOCATION: 2..541
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 1 5 10 15	46
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro 20 25 30	94
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile 35 40 45	142
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC His Pro Ala Ala Ser Leu Glu Trp Arg Asa Thr Ser Gly Leu Tyr Val 50 55 60	190
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp 65 70 75	238
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT Val lie Leu His Thr Pro Gly Cys lie Pro Cys Val Gln Asp Gly Asn 80 85 90 95	286
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	334

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105

110



Val	: GGA : Gly	Ala	ACC Thr 115	* ***	GCT Ala	TC3 Ser	ATA Ile	CGC Arg 120	AGT Ser	CAT His	GTG Val	GAC Asp	CTA Leu 125	TTA Leu	GTG Val		382
GGC Gly	GCG Ala	GCC Ala 130	****	ATG Met	TGC Cys	TCT Ser	GCG Ala 135	CTC	TAC Tyr	GTG Val	GGT Gly	GAC Asp 140	ATG Met	TGT Cys	GGG Gly		430
GCT Ala	GTC Val 145	TTC Phe	Leu	GTG Val	GGA Gly	CAA Gin 150	GCC Ala	TTC Phe	ACG Thr	TTC Phe	AGA Arg 155	510 CCI	CGT Arg	CGC Arg	CAT His		478
CAA Gla 160	ACG Thr	GTC Val	CAG Gln	ACC Thr	TGT Cys 165	AAC Asn	TGC Cys	TCG Ser	Leu	TAC Tyr 170	CCA Pro	GGC GGC	CAT His	Leu	TCA Ser 175		526
			ATG Met					-								•	541

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
115 120 - 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 140



Val 145	Phe	Leu	Val	Gly	Gla 150	Ala	₽ħe	Thr	Phe	Arg 155	Pro	Arg	Arg	His	Gla 160	
Thr	Val	Gln	Thr	Cys 165	Ast	Cis	Ser	Leu	Tyr 170	Pro	Glγ	His	Leu	Ser 175	Gĵλ	
His	Arg	Mes	Ala 190													
(2)	INFO	RMAT	CION	FCR	SEQ	ID 3	IG: 2	13:								
	(1)	(A (E	UENC L) LE L) TY L) ST L) TO	ngt: (Pe : Trani	i: 54 nucl	il ba .eis :SS:	se p acid sing	airs !	.							
	(11)	MOL	.zcv	E T	?E:	CDNA										-
	(iii)	HYE	CTHE	TIC	د:ت	ic							٠			
	(111)	ANT	:I-SE	INSE :	NC		•									
	(vii)		ŒDIA 6) CI				.10									••
	(ix)	(2	ATURE A) NA B) LO	ME/3			541									
	(xi)	SEC	30331C	E DE	ESCR:	: ? 710	CM: S	SEQ I	10 M): 23	S :					
			TT CC						la A					s G		4€
			CTT Leu													94
			TTT Pne 35													142
			GCT Ala													190
			GAC Asp												GAC Asp	238
GTT	ልሞፕ	ርፕር	Cac	GCG	CCC	GGC	TCT	GTA	ССТ	TGT	GTC	CAG	GAC	GGC	AAT	236

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90

Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn

85

9638693.081500 PCT/EP94/01323

ACC	Ser	Thr	TGC Cys	100 Lab	inr	619 619	GTA Val	ACA Thr	CCT Pro 105	Thr	GTG Val	GCA Ala	GTC Val	AGG Arg 110	TAC Tyr	334
GTC Val	GGG	GCX Ala	ACC Thr 115	Thr	GCT Ala	TCS Ser	ATA Ile	CGC Arg 120	AGT Ser	CXT Kis	GTG Val	GAC Asp	CTG Leu 125	TTA Leu	GTA Val	382
GCC	GCG Ala	GCC Ala 130	ACG Thr	ATG Met	TGC Cys	TCT Ser	GCG Ala 135	CTT	TAC Tyr	GTG Val	ely Get	GAT Asp 140	ATG Met	TGT Cys	GGG Gly	430
GCC Ala	GTC Val 145	TTC Phe	CTC	GTG Val	GGA Gly	CAA Gla 150	GCC Ala	TTC Phe	ACG Thr	TTC Phe	AGA Arg 155	CCC Pro	CGC Arg	CGC Arg	CAT His	478
CAA Gl:: 160	ACG Thr	GTC Val	CAG Gln	ACC Thr	TGT Cys 163	AAC Asa	TGC Cys	TCG Ser	Leu	TAC Tyr 170	CCA Pro	GGC Gly	CAT His	CTT	TCA Ser. 175	526
			ATG Me:													541

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly

uyoskakage1500

115	120	12:
T T 3	140	-

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140

Val Ph Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 163

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly 155 170 175

His Arg Met Ala

180

- (2) INFORMATION FOR SEQ ID NO: 25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (3) TYPE: nucleic acid-
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-19

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..541
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
- C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC
 Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 1 5 10 15
- GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC 94
 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro
 20 25 30
- GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC

 142
 Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile

 35
 40
 45
- CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC

 His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val

 50

 60
- CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC

 Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp

 70

 75



GTT Val 80	ATT	ren	CAC His	GCG Ala	Pro 85	GGC	TGT Cys	GTA Vạl	CCT Pro	TGT Cys 90	GTC Val	CAG	yab GYC	GC	AAT Asn 95		286
ACG Thr	TCT Ser	ACA Thr	TGC Cys	TGG Trp 100	ACC Thr	Pr CCA	GTA Val	ACA Thr	Pro 105	ACA Thr	GTG Val	GCA Ala	GTC Val	AGG Arg 110	TAC Tyr		334
GTC Val	elà eee	GCX Ala	ACC Thr 115	ACC Thr	GCT ALa	TCG Ser	ATA Ile	CGC Arg 120	AGT Ser	CAT Eis	GTG Val	GAC Asp	CTG Leu 125	TTA Leu	GTA Val		382
G1 y	GCG Ala	GCC Ala 130	ACG Thr	ATG Mec	TGC Cys	TCT Ser	GCG Ala 135	CTT Leu	TAC Ty -	GTG Val	GGT Gly	GAT Asp 140	ATG Met	TGT Cys	GGG Gly		430
YTE	GTC Val 145	TTC Phe	CTC Leu	GTG Val	GGA Gly	CAA Gla 150	GCC Ala	TTC Phe	ACG Thr	TTC Phe	AGA Arg 155	Pro CCC	Arg	CGC Arg	CAT His	•	478
CAA Glm 150	ACG Thr	GTC Val	CAG Gln	ACC Thr	TGT Cys 165	AAC Asn	TGC Cys	TCG Ser	Leu	TAC Tyr 170	510 CCY	GJÀ GGC	CAT His	CTT	TCA Ser 175		525
GGA (•	541

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15

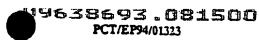
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45 .

Pro Ala Ala Gly Leu Glu Trp Arg Ast Thr Ser Gly Leu Tyr Val Leu
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

The Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90 95



Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly 115 120 125	•
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 140	
Val Phe Leu Val Gly Glm Ala Phe Thr Phe Arg Pro Arg Arg His Glm 145 150 155 160	
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly 165 170 175	
His Arg Met Ala 180	
(2) INFORMATION FOR SEQ ID NO: 27:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 541 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MCLECULE TYPE: CDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(vii) IMMEDIATE SOURCE: (B) CLONE: BR33-1-20 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2541	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	
C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 1 5 10 15	45
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro 20 25 30	94
GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile 35 40 45	142
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190

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60

His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val 55



Leu	ACC Thr 65	AAC Asn	GAC Asp	TGT Cys	TCC Ser	AAT Asn 70	AGT Ser	AGT Ser	ATT	GTG Val	TAT Ty= 75	GAG Glu	GCC Ala	GAT Asp	GAC Asp	238
GTT Val 80	ATT Ile	CTG Leu	CAC His	Ala GCG	CCC Pro 85	GGC Gly	TGT Cys	GTA Val	Pro CCI	TGT Cya 90	GTC Val	CAG Gln	GAC Asp	GGC Gly	AAT Asn 95	286
ACS Thr	TCT Ser	ACA Thr	TGC Cys	TGG Trp 100	ACC Thr	Pro Pro	GTA Val	ACA Thr	CCT Pro 105	ACA Thr	GTG Val	GCA Ala	GTC Val	AGG Arg 110	TAC Tyt	334
GTC Val	GGG Gly	GCX Ala	ACC Thr 115	ACC Thr	GCT Ala	TCG Ser	ATA Ile	CGC Arg 120	AGT Ser	CAT His	GTG Val	GAC Asp	CTG Leu 125	TTX Leu	GTA Val	382
GGC Gly	GĊG Ala	GCC Ala 130	ACG Thr	ATG Mes	TGC Cys	TCT Ser	GCG Ala 135	CTT Leu	TAC Tyr	GTG Val	GGT Gly	GAT Asp 140	ATG Met	TGT Cys	GGG Gly	430
GCC Ala	GTC Val 145	TTC Phe	CTC Leu	GTG Val	GGA Glγ	CAA Gl:: 153	GCC Ala	TTC Phe	ACG Thr	TTC Phe	AGA Arg 155	CCC	CGC Arg	CGC	CAT His	479
CAA Glm 160	ACG Thr	GTC Val	CAG Gln	ACC Thr	TGT Cys 165	AAC Asa	TGC Cys	TCG Ser	CTG Leu	TAC Tyr 170	CCY Sto	GGC Gly	CAT His	CTT Leu	TCA Ser 175	526
GGA Gly																541

- (2) INFORMATION FOR SEQ ID NO: 29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

Ile	Leu	His	ALE	25 28	Gly	Càe	Val	Pro	90	Val	Gla	Asp	Gly	Asn 95	Thr	
Ser	Thr	Cys	100	The	PTO	Val	Thr	Pro 105	Thr	Val	Ala		Arg 110	Tyr	Val	
Gly	Ala	Thr 115	Thr	Ala	Ser	Ile	753 750	Ser	발효	Val	ÇZÁ	Leu 125	Leu	Val	G ₂ y	
Als	Ala 130	<u>:</u>	Met	Суз	Ser	Ala 135	Leu	<u>:\:</u>	Val	Gly	کچې 140	Mes	Cys	Gly	Ala	
Val 145	Phe	Leu	Val	Gly	Gln 150	بنه	Phe	Thr	Phe	Arg 155	Pro	yzâ	Arg	His	Gl: 160	
Thr	Val	Gln	Thr	Cys 163	Asn	C'na	Ser	Leu	Ty= 170	Pro	GJŸ	His	Leu	Ser 175	Gly	
His	Ezy	Met	Ala 180													•
(2)	INFO	RMA	TON	FOR	SEQ	13 N	10 : Z	29:								
	(i)	() ()	(UENC L) LE L) TY C) SI D) TO	ngti Pe: Rant	i: 28 nucl	7 ba .eic :SS:	se ; acid	airs !	•							٠
	(ii)	MOI	ECUL.	E T	Æ:	CENA	•									
(iii)	HYE	OTHE	TIC	L: N	iC										
(iii)	AN:	TI-SE	NSE :	NO											
• (vii)	_	EDIA () Cl	-			1	•								
	(ix)	(A	TURE () NA () LC	ME/X			187									
	(xi)	SEC	UENC	E D	SCRI	PTIC)N: S	EQ I	מ ס): 29):					•
			tb e													47
CAC Kis	TTT Phe	CTG Leu	TCA Ser	CAG Gln 20	ACT Thr	aag Lys	CAG Gla	CAG Gln	GGA Gly 25	CTC Leu	AAC Asn	TTC Phe	TCG Ser	TTC Phe 30	CTG Leu	95
ACT	GCC	TAC	CAA	GCC	ACT	GTG	TGC	GCT	CGC	GCG	CAG	GCT	сст	CCC	CCA	143

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40 AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA

Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro

35

Ser Trp Asp Glu Met	Tro Lys Cys Leu	Val Arg Leu Lys Pro Thr Leu
50	\$5	60

CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu
65 70 75

120

- ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA

 11s Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser

 80 90 95
- (2) INFORMATION FOR SEQ ID NO: 30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 1 5 10 15

Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr 20 25 30

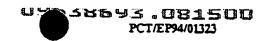
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Ser 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His 50 60

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 65 70 75

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser 85 90 95

- (2) INFORMATION FOR SEQ ID NO: 31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 (B) CLONE: HD10-1-25



(ix) FEATURE	:
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(A) NAME/KEY: CDS
(B) LOCATION: 3..401

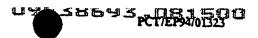
(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

								754			••						
TC ·	CAA Gln 1	AAT Asa	GAA Glu	ATC Ile	TGC Cys 5	TTG Leu	ACA Thr	CAC Eis	310 CCC	GTC Val 10	aca The	AAA Lys	TAC Tyr	ATT	ATG Met 15		47
GCA Ala	TGC	ATG Met	TCA Ser	GCT Als	Asp	Leu	GAR Glu	GTA	ACC Thr 25	The	AGC Se:	ACC Thr	TEP	GTG Val	TIG Leu		95
CTT	GGA Gly	GGG Gly	GTC Val	Lev	GCG Ala	GCC Ala	CTA Leu	GCG Ala 40	Ala	TAC	TGC Cys	: TTG : Leu	Ser 45	Val	GGC	-	143
TGC	GTT Val	GTA Val 50	Ile	GTG Val	GGT Gly	CAT His	Ile 55	Glu	CTG	GGG G1y	GGC Gly	AAG Lys	220	GCA Ala	CTC Leu		191
		Asp					Tyr					Glu			GAG Glu		239
TGC Cys 80	TCG Ser	CAA Gln	GCC Ala	GCC Ala	CCA Pro 85	TAC	ATC Tle	GAA Glu	CAA Gln	GCT Ala 90	Gla	GTA Val	ATA Ile	GCC Ala	CAC His 95		287
CAG Gla	TTC Pha	AAG Lys	GAG Glu	AXA Lys 100	Ile	CTT	GGA Gly	CTG Leu	CTG Leu 105	CAG Gln	CGA	GCC Ala	ACC	CAA Glm 110	CAA Glm		335
				Glu										Leu	GAA Glu		383
					CAT His												401

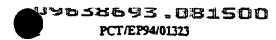
(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala 1 5 10 15



Cys	Met	Ser	Ala 20	Asp	Leu	Glu	Val	Thr 25	Thr	Ser	Thr	īrp	Val 30		Leu	
Gly	Gly	Val 35	Leu	Ala	Ala	Leu	Ala 40	Ala	Tyr	Cys	Leu	Se: 45	Val	Gly	Cys	
Val	Val 50	Ile	Val	Gly	His	Ile 55	Glu	Leu	Gly	GŢŸ	60 Lys	Pro	Ala	Leu	Val	
PT0 65	Asp	Lys	Glu	Val	70	عات	Gla	Gln	Tyr	ծsp 75	Glu	Mec	Glu	Glu	Cys 80	
Ser	Gln	Ala	Ala	P20 85	Tyr	Ile	Glu	Gla	Ala 90	Gln	Val	Ile	Ala	His 95	Gln	
Phe	Lys	Glu	Lys 100	Ile	Leu	GΊΥ	Leu	Leu 105	Gla	Arg	λla	Thr	Gln 110	Gla	Glm	
		115	Glu Lys		Val	Ile	Ala 120	Ser	Asn	ŢŢ	Gla	Lys 125	Leu	Glu	Thr	
	130		'ICN		570	73. N										
. (1	(ii) iii) iii) vii)	(A (E (C) (D) MOL HYP ANT IMM (B	CUENCE () LE () TY () TO () TURE () NAW () LOO () LOO ()	NGTH PE: RAND POLO E TY TICA NSE: TE S ONE:	EY:	l ba eic :55: line cDNA TO	se pacification of the second	airs								
			UENC											•		
C C	AA A In A	AT G. sn G.	AA A' lu I:	TC To	GC T ys L 5	TG A eu T	CA C hr H	AC C is P	zo A	TC A al T 10	CA A hr L	AA T YS T	yr I	TT A	ITG let 15	47
CA 1	rgc :	ATG '	TCA (Ser)	GCT (Ala . 20	GAT (Asp)	CTG (Leu (GAA - Glu	GTA Val	ACC Thr 25	ACC Thr	AGC Ser	ACC Thr	TGG Trp	GTG Val 30	TTG Leu	95
TT	GGA (GG (GTC (CTC (GCG (GCC (CTA	GCG	GCC	TAC	TGC	TTG	TCA	GTC	GGC	143



	Gly	Gly	Val 35	Leu	λia	Ala	Leu	시a 40	Ala	Tyr	Cys	Leu	Ser 45	Val	Gly	
TGC Cys	GTT Val	GTA Val 50	ATC Ile	GTG Val	GGT Gly	CAT His	ATC Ile 55	GAG Glu	CTG Leu	GGG Gly	GGC Gly	aag Lys 60	510 CC3	GCA Ala	CTC Leu	191
GTT Val	Pro 65	GAC Asp	AAG Lys	GAG Glu	GT3 Val	TTG Leu 70	TAT Tyr	CAA Gln	CAG Gln	TAC Tyr	GAT Asp 75	GAG Glu	ATG Met	GAG Glu	gag Glu	239
TGC Cys 80	TCG Ser	CAA Gln	GCC Ala	GCC Ala	CCA Pro 85	TAC Tyr	ATC Ile	Gàà Glu	GJ::	GCT Ala 90	CAG Gln	GTA Val	ATA Ile	GCC Ala	CAC His 95	237
CAG Gln	TTC Phe	AAG Lys	GAG Glu	lys Lys	ATC Ile	CTT Leu	GGA Gly	CTG Leu	CTG Leu 105	CAG Gln	yzd CGY	GCC Ala	acc Thr	CAA Gln 110	CAA Gln	335
				GAG Glu												352
				AAG Lys												401
(2)	INFO	ORMA!	rton	2 02	550	TO A										
				rua	~~~	1-0	10: 3	• • •								
		(i) S (; (E	EQUE L) LE B) T	DICE ENGT: (PE: (POLC	CHAS : 13 amir	PACTE 33 an	ERIST mino mid	rics:			,					
	,	(i) {} {} []	SEQUE LE B) To	DICE INGT: (PE :	CHAI : 1: amir :GY:	PACTE 33 an 10 ac 1ine	ERIST mino mid mar	rics:								
	(ii)	(i) (i) (i) (i) (i) (i) (i) (i) (i) (ii) (ii) (ii) (ii) (iii) (iii	SEQUE () LE () To LECUE	DICE INGTA (PE: OPOLO	CHAS E: 13 amir GGY:	PACTE 3 and ac 1 inc	ERIST mino mid mid mar mein	TICS: ació	s): 3 4	.					
	(ii)	(i) (i) (i) (i) (i) (i) (ii) (ii) (ii)	SEQUENC	DICE INGTH (PE: DPOLC LE TI	CHAS : 13 amir >GY: :FE:	PACTE 33 an 10 ac 1ine prot	ERIST mino cid ear tein	TICS: acid	is .			Tyr	Ile	Met 15	Ala	
Gla 1	(ii) (xi) Asn	(i) S (i) (i (i) (ii MOI SEC	SEQUE () LE () TO LECUI QUENC Ile	ENCE ENGTH (PE: OPOLO LE TI LE DI Cys	CHAS E: 13 amir OGY: CFE: ESCRI	PACTE 3 and according 1 inc 1 prot 1 prot 1 prot 1 prot	erising idear lein	FICS: acid	D NO	Thr	Lys	-		15		
Gla 1 Cys	(ii) (xi) Asn Met	(i) (i) (i) (i) (ii) (ii) (iii) (iii	SEQUENCE ILECUIA ALA 20	ENCE ENGT: (PE: DPOLC LE TI LE DS Cys 5	CHAI H: 13 amir GGY: FFE: SCR1 Leu	PACTE 33 an 10 ac 1 ine prot PTIC Thr	ERIST mino rid ear mein ON: S His	FICS: acid	D NO Val 10	Thr Ser	Lys Thr	Trp	Val 30	15 Leu	Leu	
Gla 1 Cys	(ii) (xi) Asn Met Gly	(i) § (i) § (i) (ii) (ii) (iii) (iii	EEQUE Ala 20 Lecur	Cys Asp	CHAI amir GGY: CFE: Leu Leu	ACTI 33 an 100 ac 11ne prot Thr Glu Leu	PRIST nine rid ear sein N: S His Val	FICS: acid	D NO Val 10	Thr Ser Cys	Lys Thr Leu	Trp Ser 45	Val 30 Val	15 Leu Gly	Leu Cys	
Gla 1 Cys Gly Val	(iii) (xi) Asn Met Gly Val 50	(i) (i) (i) (i) (ii) (ii) (iii) (iii	EEQUENC LECUI QUENC LECUI LECUI LECUI LECUI Val	DICE INSTR (PE: OPOLO DE TI DE DE Cys S Asp	CHAI amir GY: FE: Leu Leu Aia	Protection of the control of the con	cristing control of the cristi	Thr 25	Val 10 Thr	Thr Ser Cys	Lys Thr Leu Lys 60	Trp Ser 45	Val 30 Val Ala	Leu Gly Leu	Leu Cys Val	

SUBSTITUTE SHEET (RULE 26)

Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln

100

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr 115 120 125

Phe Trp His Lys His

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (Vii) IMMEDIATE SCURCE:

(B) CLONE: 9R36-20-164

(ix) FEATURE:

80

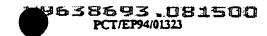
- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TC	CAA Gln 1	AAT Asn	GAA Glu	ATC Ile	TGC Cys S	TTG Leu	ACA Thr	CAC His	CCC Pro	ATC Ile 10	ACA Thr	aaa Lys	TAC Tyt	ATC Ile	ATG Met 15	47
GCA Ala	TGC Cys	Mes	S TCA	GC: Ala 20	Asp	CTG Leu	GAA Glu	GTA Val	ACC This	The	AGC Sei	ACC The	Tr	GTT Val	TTG Leu	95
CTT	GGA Gly	GGG Gly	GTC Val	Leu	GCG Ala	GCC Ala	CTA Leu	GCG Ala	Ala	TAC	TGC Cys	TTG Leu	TCA Ser 45	Val	GGT Gly	143
TGT Cys	GTT Val	GTG Val	Ile	GTG Val	GGT	CAT His	ATC Ile 55	Glu	CTC Leu	GGG Gly	GGC Gly	AAG Lys	Pro	GCA Ala	ATC Ile	191
GTT Val	CCA Pro 65	Asp	lys	GAG Glu	GTG Val	TTG Leu 70	Tyr	CAA Gln	CAA Glm	TAC	GAT Asp 75	Glu	ATG Met	GAA Glu	GAG Glu	239
TGC Cys	TCA Ser	CAA Gln	GCT Ala	GCC Ala	CCA	TAT Tyr	ATC Ile	GAA Glu	CAA Gln	GCT Ala	CAG	GTA Val	ATA	GCT Ala	CAC His	297

SUBSTITUTE SHEET (RULE 26)

CAG TTC AAG GGA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA



Gln Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Try Gln Lys Leu Glu
115
120
125

GCT TTT TGG CAC AAG CAT Ala Phe Trp His Lys His 130

401

- (2) INFORMATION FOR SEQ ID NO: 36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 1 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Mer Glu Glu Cys 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gin Val Ile Ala His Gln 85 90 95

Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala 115 120 125

Phe Trp His Lys His

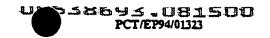
- (2) INFORMATION FOR SEQ ID NO: 37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

								14	.0							
	(11) MC	DLECT	TLE 1	TYPE:	CDN	A									
((iii) R2	(20T3	ETIC	AL:	NO										
((iii) AN	TI-S	ENSE	: NO)										
(vii				SOUR : BR		0-16	6								
	(ix	(AME/	KEY:											
	(x±)) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	N CI	0: 3	7:					
TC C.	AA I la I	AAT Asn	GAA Glu	ATC Ile	TGC (Cys)	TTG Leu	ACA Thr	CAC His	CCC . Pro	ATC Ile 10	ACA Thr	aaa Lys	TAC . Tyr	ATC Ile	ATG Mei 15	47
GCA '	TGC Cys	ATG Mec	TCA Ser	GCT Ala 20	Asp	CTG Leu	GAA Glu	GTA Val	ACC Thr 25	ACT Thr	AGC Ser	ACC Thr	TGG TYP	GTT Val 30	Leu	95
CTT (GGA Gly	GGG GLY	GTC Val 35	CTC	GCG Ala	GCC Ala	CTA Leu	GCG Ala 40	11a	TAC Tyr	TGC	TTG Leu	TCA Ser 45	GTC Val	GIY	143
TGT (GTT Val	GTG Val 50	ATT Ile	GTG Val	GGT Gly	CAT His	ATC Ile 55	GAG Glu	CTG Leu	GGG Gly	GGC Gly	AAG Lys 60	SLO	GCA Ala	ATC Ile	191
GTT (CCA Pro 65	GAC Asp	AAA Lys	GAG Glu	GTG Val	TTG Leu 70	TAT Ty=	CAA Gla	CAA Gln	TAC Tyr	GAT Asp 75	GAG Glu	ATG Met	GAA Glu	GAG Glu	239
TGC 1 Cys s	ICA Ser	CAA Gln	GCT Ala	GCC Ala	CCA Pro 85	TAT Tyr	ATC Ile	GAA Glu	CAA Glm	GCT Ala 90	CAG Gln	GTS Val	ATA Ile	GCT Ala	CAC His 95	237
CAG 1	ITC Phe	AAG Lys	GAA Glu	AAA Lys 100	GTC Val	CTT	GGA Gly	TTG Leu	CTG Leu 105	CAG Gln	CGY	GCC Ala	ACC Thr	CAA Gln 110	CAA Gln	335
CAA G	GCT Nia	GTC Val	ATT Ile 115	GAG Glu	CCC Pro	ATA Ile	GTA Val	ACT Thr 120	ACC Thr	AAC Asi	TGG	CAA Glm	AAG Lys 125	CTT Leu	GAG Glu	383
GCC TALL P																431

(2) INFORMATION FOR SEQ ID NO: 38:

130

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids



- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 1 5 10

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln 85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gin Arg Ala Thr Gin Gin Gin 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala 115 120 125

Phe Trp His Lys His

- (2) INFORMATION FOR SEQ ID NO: 39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-165

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..401
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

	1	ASN	GAA Glu	116	Cys 5	Leu	Thr	His	Pro	Ile 10	Thr	Lys	ΙλΞ	Ile	Mec 15	47
750	. Cys	mes	. ser	20	Asp	Leu	Glu	. Val	7hz 25	The	Sez	Thr	ırb	Vai		95
CTT	GGA Gly	GGG Gly	GTC Val 35	Leu	GC3 Ala	GCC Ala	CTA Leu	GC3 Ala 40	λla	TAC	TGC	TTG Leu	7CA Ser 43	GTC Val	GGT Gly	143
TGT Cys	GTT Val	GTG Val 50	ATT	GTG Val	GGT Gly	CAT His	ATC Ile 55	GAG Glu	CTG Leu	GGG Gly	GGC	AAG Lys 60	CCG Pro	GCX Ala	ATC	191
GTT Val	CCA Pro 65	GAC Asp	AAA Lys	GJ 11	GTG Val	TTG Leu 70	TAT Tyr	CAA Gla	CAĄ Gln	TAC Tyr	GAT Asp 75	GAG Glu	ATG Met	GAA Glu	GAG Glu	. 239
TGC Cys 80	TCA Ser	CAA Gln	GCT Ala	GCC Ala	CCA Pro- 85	TAT Tyr	ATC Ile	GAA Glu	CAA	GCT Ala 90	CAG Gla	GTA Val	ATA Ile	GCT Ala	CAC His 95	297
CAG Glm	TTC Phe	AAG Lys	GAA Glu	AAA Lys 100	GTC Val	CTT Leu	GGA Gly	TTG Leu	CTG Leu 105	CAG Gln	CGA	GCC Ala	ACC Thr	CAA Glm 110	CAA Gla	335
CAA Glm	GCT Ala	GTC Val	ATT Ile 115	GAG Glu	CCC Pro	ATA Ile	GTA Val	ACT Thr 120	ACC Thr	AAC Asn	1.15 1.03	CAA Gln	AAG Lys 125	CTT Leu	GAG Glu	383
			CAC His													401

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Glm Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

WO 94	/2560	1				•		12			اد اليا					EP94/0	
Va!	Val 50	Ile	Val	Gly	His	Ile 55	Glu			Gly	Lys 60	Pro	Ala	Ile	Val		
Pro 63	Asp	Lys	Glu	Val	Leu 70	ī/ī	Gln	Gln	Tyr	Asp 75	Glu	Mec	Glu	Glu	Cys 80		
Ser	Gln	Ala	Ala	219 28	ī'n	Ile	Glu	Gln	ኢ la 90	Gln	Val	Ile	Ala	His 95	Gln		
?te	Lys	Glu	Lys 100	Va:	Leu	Gly	Leu	Leu 105	Gla	λrg	λia	Thr	Gin 110	Gla	Gln		
Ala	Val	Ile 115	Glu	Pro	Ile	Val	Thr 120	Thr	Asn	ţxp	Gla	Lys 125	Leu	Glu	Ala		
Phe	Trp 130	His	Lys	His													
		SE() (2) (2)	OUENC L) LE B) T' C) S'	FOR CE CE ENGTE CPE: CRANE OPOLO	EARAG E: 50 nucl	TER: 09 ba .eic SS:	STIC use p acid sing	IS: pairs	5								
,				E T			•										
				TICA ENSE:		10											
. (vii)			NTE S LONE :													
	(ix)	(A		: WE/X CATI			109										
	(xi)	SEC	UENC	E DE	SCRI	PTIC	N: 5	EQ I	מא כב): 42	. :						
CC A	TG A et S	GC A er I	CG A	LST C	CT A	ys E	CT C	iaa a Sla a	iga a	ys T	cc a	ka Key	AGA X	lac :	acc Thr		47

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gla	Arg	-	Thr	Lys	Yza .	Asn	Thr	
	1				5					10					15	
AAC	CGT	CGC	cca	CAG	GAC	GTC	AAG	TTC	CCG	GGC	GGT	GGT	CAG	ATC	GTT	95
				Gln												
				20					25		•	•		30		
GGC	GGA	GIT	TAC	TTG	TTG	CCG	CGC	AGG	GGC	CCT	AGG	ATG	GGT	GTG	CGC	143
Gly	Gly	/ Val	LTyr	Leu	Leu	Pro	Arg	-Arg	Gly	Pro	Arg	Met	Gly	Val	Arg	
			3 9	5				40					45			
GCG	ACT	CGC	AAG	ACT	TCG	GAA	CGG	TCG	CAA	. ccc	CGT	GGA	CGG	CGT	CAG	191
Ala	The	Arc	Lys	The	Ser	Glu	Arq	Ser	Gln	Pro	Ara	Glv	Arc	2-0	Gla	

55

60

CCT Pro	ATT Ile 65	Pro	AAG Lys	GCG Ala	CGC	CAG Glm 70	S20 CCC	ACG Thr	GGC Gly	CGG Arg	TCC Ser 75	TEG TEG	GGT Gly	CAA Gln	CCC Pro	2:	39
GGG Gly 80	ı'nz	Pro	TGG	Pro	CTT Leu 85		GCC Ala	AAT Asn	GAG Glu	GGC Gly 90	CTC	GGG Gly	TGG T:p	GCA Ala	GGG Gly 95	21	87
1.tb	CTG Leu	CTC	TCC Ser	CCT Pro 100	CGY	G1y GGC	TCT Ser	CGG ATG	CCT Pro 105	TAA Taa	TGG Trp	GGC Gly	Sto	AAT ASD 110	GAC ÇeA	33	35
CCC	CGG Arg	CGA Arg	AAA Lys 115	TCG Ser	CGT Arg	AAT Asn	TIG Leu	GGT Gly 120	AAG Lys	GTC Val	ATC Ile	gat Asp	ACC Thr 125	CTA Leu	ACG Thr	36	13
TGC Cys	GGA Gly	TTC Phe 130	GCC Ala	GAT Asp	CTC Leu	ATG Met	GGG Gly 135	TAT Tyr	ATC Ile	CCG Pro	CTC Leu	GTA Val 140	GGC Gly	GGC Gly	DE0 CCC	43	11
ATT	GGG Gly 145	Gly	GTC Val	GCA Ala	Arg	GCT Ala 150	CTC CTC	GCA Ala	CAC His	GGT Gly	GTG Val 155	AGG Arg	GTC Val	CTT Leu	GAG Glu	47	9
			AAC Asn													50	9

- (2) INFORMATION FOR SEQ ID NO: 42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gin Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp

Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
			100					105		•			110	•	

Arg Arg Lys Ser Arg Asm Leu Gly Lys Val Ile Asp Thr Leu Thr Cys 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Île Pro Leu Val Gly Gly Pro Ile 130 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu
165

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLETULE TYPE: cONA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE: (B) CLONE: PC-2-6
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CC ATG	AGC ACG	AAT CCT A	WAX CCT CAX	AGA AAA ACC	AAA AGA AAC	ACC 47
Met	Ser Thr	Asn Pro L	Lys Pro Gla	Arg Lys Thr	Lys Arg. Asn	Thr
1		5		10		15

AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT

Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val

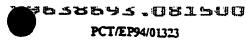
20
25
30

GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC

143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg

45

GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG 191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln



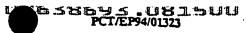
		•				•		1	32 ·						PCT/EP	14/01323	
Pro	T ATT	SIO	Lys	GCG Ala	Arg CGC	CAG Gln 70	520 CCC	ACG Thr	GGC Gly	CGG Arg	TCC Ser 75	11p	GCT	CAA Gln	CCC Pro	239	
GG(Gl ₃ a(TAC Tyr	Pro	ISP	CCC	CTT Leu 85	TAC Tyr	GCC Ala	AAT Asn	GAG Glu	GGC Gly 90	Leu	GGG	TGG Trp	GCA Ala	GGG Gly 95	287	
TGG	CTG Leu	CTC	TCC	CCT PTO 100	yrg	GGC Gly	TCT Ser	CGG ATG	CCT Pro 105	AAT Asn	TGG Trp	GLY	510 CCC	AAT Asn 110	GAC Asp	335	
Pro	CGG Arg	CGA	AAA Lys 115	TCG Ser	CGT Arg	AAT Asn	TTG Leu	GGT Gly 120	AAG Lys	GTC Val	ATC Ile	GAT Asp	ACC Thr 125	CTA Leu	ACG Thr	.383	
TGC Cys	GGA Gly	TTC Phe 130	GCC ¹	GAT Xsp	CTC Leu	ATG Mes	GGG Gly 135	TAT Tyr	ATC Ile	CCG Pro	CTC Leu	GTA Val 140	GLY	GGC Gly	CCC Pro	431	
ATT	GGG Gly 145	GGC Gly	GTC Val	GCX Ala	AGG AIG	GCT Ala 150	CTC CTC	GCA Ala	CAC His	GGT Gly	GTG Vai 153	AGG Arg	GTC Val	CTT Leu	GAG Glu	479.	•
GAC Asp 160	GGG Gly	GTA Val	AAC Asn	TAT Tyr	GCA Ala 165	ACA Thr	G17 GGG	AAT Asn	TTA Leu							509	
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	IC: 4	4:									
	(K) E)	EQUE L) LE L) TY D) TO	NGTH PE:	: 16 amin	9 am	ino id										
	(<u>ii</u>)	MOL	ECIL	E TY	PE:	pret	ein										
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	ОИ C	: 44	:						
Met 1	Ser	Thr	Asn	Pro 5	Lys	Pro	Gln	Arg	Lys 10	Thr	Lys	Arg	Asn	Thr 15	Asn		
Arg	Arg	Pro	Gln 20	Asp	Val		Phe			Gly	Gly	Gln	Ile	Val	Gly		

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 70

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90



	•••				•		. 1	33						PCT/	EP94/(11323
Leu Le	u Ser	Pro 100	Arg	Gly	Ser	Arg	PT0 105	Asn	ITP	Gly	Pro	Asn 110	qsA	Pro		
Arg Ar	g Lys 115	Ser	Arg	Asn	Leu	Gly 120	Lys	Val	Ile	Asp	Thr 125	Leu	Thr	Cys		
Gly Ph	e Ala O	Asp	Leu	Met	Gly 135	Tyr	Ile	Pro	Leu	Vai 140	Gly	Gly	Pro	Ile		
Gly Gl 145	y Val	Ala	yzâ	Ala 150	Leu	aند	His	Gly	Val 155	کتع	Val	Leu	Glu	Asp 160		
Gly Va	l Asn	Tyr	Ala 165	Thr	GŢĀ	Asn	Leu									
(2) IN	forma:	rion	FOR	SEQ	ID 1	10: 4	15:									
(:	(2	A) Li 3) Ti 2) Si	ce ce engte (Pe : [rani opolo	1: 50 מעכנ מעכנים	80 ba Leic ESS:	se p acid	pairs i	3							•	
(i:) MOI	LECUI	LZ T	PE:	CDNA	L .										
(iii	.) HYI	?OT:13	TIC	I: N	1 0											
(iii	.) AN	CI-SE	ense:	NO												
(vii	.) IMP (E		NTE S CNE:													
(i)		() NA	:: ME/X CATI			80										
(xi) SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	: 45	:						
A ACG T Thr C	GC GG ys Gl	y Pb	C GC	C GA a As 5	T CT p Le	C AT	G GG	G TA y Ty 1	z Il	C CC e Pr	G CT o Le	C GT.	1 G1	С У 5		46
GGC CCC Gly Pro	ATT	GGG Gly	GGC Gly 20	GTC Val	GCA Ala	AGG Arg	GCT Ala	CTC : Leu . 25	GCA Ala	CAC	G17 G3T	GTG . Val .	AGG Arg 30.	Val		94
CTT GAG Leu Glu	GAC Asp	GGG Gly 35	GTA Val	AAC Asn	TAT Tyr	GCA Ala	ACA Thr 40	GGG . Gly .	AAT Asn	TTA Leu	CCC ·	GGT Gly 4	TGC Cys	TCT Ser		142
TTC TCT Phe Ser													CCG	GCC		190

SUBSTITUTE SHEET (RULE 26)

TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT

Ser	Ala 65	Val	Pro	ī'n	Arg	Asn 70	Ala	Ser	Gly	Ile	Tyr 75	His	Val	Thr	Asn		
GAT Asp 80	Cys	CCA Pro	AAC Asn	TCT Ser	TCC Ser 85	ATA Ile	GTC Val	TAT Tyr	GAG Glu	GCA Ala 90	TAÐ geA	AAC Asa	CTG Leu	ATC Ile	CTA Leu 95		286
CAC His	GCA Ala	Sto	GGT Gly	TGC Cys 100	GTG Val	510 CCI	TGT Cys	GTC Val	ATG Mec 105	ACA Thr	GGT Gly	AAT Asn	GTG Val	AGT Ser 110	AGA Arg		334
TGC Cys	TGG	GTC Val	CAA Gln 115	ATT Ile	ACC Thr	CCT Pro	ACA Thr	CTG Leu 120	TCA Ser	GCC Ala	PIO CCG	AGC Ser	CTC Leu 125	gga Gly	GCA Ala		392
GTC Val	AC3 Thr	GCT Ala 130	CCT PTO	CTT Leu	CGG Arg	AGA Arg	GCC Ala 135	GTT Val	GAC QaA	TAC Tyr	CTA Leu	GCG Ala 140	GGA Gly	GGG G1y	GCT Ala		430
GCC Ala	CTC Leu 145	TGC Cys	TCC Ser	GCG Ala	TTA Leu	TAC Tyr 150	GTA Val	GGA Gly	GAC Asp	GCG Ala	TGT Cys 155	GGG Gly	GCA Ala	CTA Leu	TTC Phe	•	478
TTG Leu 160	GTA Val	GGC Gly	CAA Gln	ATG Met	TTC Phe 155	ACC Thr	TAT Tyr	AGG Azg	Sio	CGC Arg 170	CAG Gln	CAC His	GCT Ala	ACG Thr	GTG Val 175		526
CAG Gln	AAC Asii	TGC Cys	AAC Asn	TGT Cys 180	TCC Ser	ATT Ile	TAC Tyr	AGT Ser	GGC Gly 185	CAT Eis	GTT Val	ACC Thr	GGC Gly	CAC His 190	CGG Arg		574
ATG Met																	580

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10

Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60



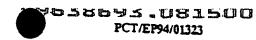
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pr Asn Ser Ser Ile Val Tyr Glu Ala Asp Asa Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Ash Val Ser Arg Cys Try Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 145 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln 170 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met 180 Ala (2) INFORMATION FOR SEQ ID NO: 47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 580 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single . (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (vii) IMMEDIATE SOURCE: (B) CLONE: PC-4-6 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2..580 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47: A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC

GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly

5

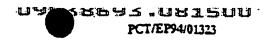
1



Gl	y P=	o Il	e Gly	y Gly 20	/ Val	Ala	. Arg	, Ala	Let 25	1 Ala 5	a Sig	s Gly	/ Val	Arg	; Val	
CT Le	T GA	G GA	GGG G1 y 3 S		AAC Asn	TAI	GCA Ala	ACA The	GI.	; AA: / As:	TTA Let	: Pro	GGT Gly	Cys	TCT Ser	142
TT: Ph	C TC	T ATO		ATT	CIT	GCT Ala	CT: Leu 55	Let	: TCG : Sez	Cha 131	CTS	ACC Thr	Val	. CCG	GCC Ala	190
TC:	GC: Ala 69		CCC Pro	TAC	CGA Arg	AAT Asn 70	GCC Ala	TCT Ser	Gly	ATT Ile	TAT Tyr 75	His	G Val	ACC Thr	AAT Asn	238
GAT Çek 80	,-	CCA Pro	AAC Asn	TCT Ser	TCC Ser 85	ATA Ile	GTC Val	TAT Tyt	GAG Glu	GCA Ala 90	GAT Çek	AAC Ast	CTG Leu	ATC Ile	CTA Leu 95	286
CAC His	GCA Ala	Sio	GGT Gly	TGC Cys 100	GTG Val	CCT Pro	TGT Cys	GTC Val	ATG Mes 105	ACA Thr	GG T Gly	AAT Ast	GTG Val	AGT Ser 110	AGA Arg	334
TGC Cys	IGG TGG	GTC Val	CAA Glm 115	ATT Ile	ACC Thr	CCT Pro	ACA Thr	CTG Leu 120	TCA Ser	GCC Ala	CC3 Pro	AGC Ser	CTC Leu 125	GGA Gly	GCA Ala	382
GTC Val	ACG Thr	GCT Ala 130	CCT Pro	CTT Leu	YZ3 CGG	AGA Arg	GCC Ala 135	GTT Val	ರ್ಷ ೧೩೦	TAC Tyr	CTA Le u	GCG Ala 140	GGA Gly	GGG Gly	GCT Ala	430
GCC Ala	CTC Leu 145	TGC Cys	TCC Ser	GCG Ala	TTA Leu	TAC Tyr 150	GTA Val	gga Gly	GAC Asp	GCG Ala	TGT Cys 155	GGG	GCA Ala	CTA Leu	TTC Phe	478
TTG Leu 160	GTA Val	GGC Gly	CAA Gln	met	TTC Phe 165	acc Thr	TAT Tyr	AGG Arg	320	CGC Arg 170	CAG Glm	CAC His	GCT Ala	Thr	GTG Val 175	525
CAG Gln	AAC Asn	TGC Cys	AAC Asn	TGT Cys 180	TCC . Ser	ATT	TAC Tyt	Se:	GGC Gly 185	CAT Eis	GTT Val	ACC Thr	Gly	CAC His 190	CGG Arg	574
ATG Met																580

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear -
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:



Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly

1 5 10 15

Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Ash Tyr Ala Thr Gly Ash Leu Pro Gly Cys Ser Phe 35 40

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys

Trp Val Gin Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Giy Ala Val

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln 165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met 180 195 190

Ala

(2) INFORMATION FCR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: PC-3-4

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

												• • •						
	1				•	5	., J	0	GIN	Arg	Lys 10	The	Ly	s Arg	j As:	ACC Thr 15		47
			•		20	- J	•	Ly:	s Pri	2	2 O CT	y Gl	y Gi	y Gl	n Il 3	C GTT e Val		95
		-		35			•	مدو	40) }	y Pz	יא כ	g Me	t G1 4	y Va 5	G CGC l Arg	_	43
GCG Ala	AC. Thi	CC Az	G A G L	AG A Ys T	CT 1 hr s	CG (GAA Glu	CGG Arg	26:	Gl:	A CCC	CG Ar	T GG G1 6	y Ar	g CG	r cag g Gln	1	91
CCT Pro	ATT	Pr	C A	AG G Ys A	CG C ia A	GC (CAG 51n 70	CCC	ACG Thr	GGC Gly	Cig Arg	TC: Se: 75	T.	G GG	T CAN Y Gl:	A CCC	. 2:	39
80	•					85	. g = .	n ia	ASR	GTA	90	Leu	Gl	/ Iri	Ala	GGG Gly 95	29	17
				10	00	., .	- ,	361	Arg	105	ASI	طئي	Gl;	' Pro	As::		33	5
	-		11	5		·y	9.1 1	Leu	120	rvs	Vai	lie	Asp	Thr 125	Leu	ACG Thr	38	3
TGC Cys	GGA Gly	Phe 130	GC: Al.	C GA a As	T CI p Le	C A	בנ נ	GG Gly	TAT Tyr	ATC Ile	CCG Pro	CTC Leu	GTA Val 140	GGC	GGC Gly	CCC	43	i
ATT (3G3 31y 145	GGC Gly	GTC Val	C GC	A AG a Ar	G G(F A)	ra L	TC eu	GCA Ala	CAC His	GCT Gly	GTG Val 155	AGG Arg	GTC Val	CTT Leu	GAG Glu	47:)
Asp (GG Sly	GTA Val	AAC Asn	TA'	T GC: T Ala	3 12	ix G	GG . ly .	AAT Asn :	Leu	CCC Pro 170	GGT Gly	Cys	TCT Ser	TTC Phe	TCT Ser 175	521	7
ATC T	TT .	ATT Ile	CTT	GC: Ala 180	, me	CT Le	C T	CG :	.ys	CTG Leu 185	ACC (Thr '	GTT Val	CCG Pro	GCC Ala	TCT Ser 190	GCA Ala	579	5
GTT C	to . CC .	TAC Tyr	CGA Arg 195	~3.	GCC Ala	TC Se	T G(r G)	-y	ATT 1 Lie 1	rat (Pyr 1	CAT (Ris 1	GTT .	ACC Thr	AAT Asn 205	GAT Asp	TGC Cya	623	I



	ححم	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCA	GAT	AAC	CTG	ATC	CTA	CAC	GCA		671
	Pro	Asn	Ser	Ser	Ile	Val	Ty	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala		
			210					215		_			220					
	CCT	GGT	TGC	GTG	cct	TGT	GTC	ATG	ACA	GGT	AAT	GTG	AGT	AGA	TGC	TGG		719
	PFO		Cys	Val	9r	Cys		Met	Thr	Gly	Asn	Vai	Ser	Arg	Cys	ŢŢ		
		225					230					235						
Ľ	GTC	CAA	ATT	ACC	CCT	ACA	CTG	TCA	GCC	CCG	AGC	CTC	GGA	GCA	GTC	ACG		767
	Val	Gln	Ile	Thr	P T0	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr		
	240					245					250					255		
				CGG														815
	Ala	Pro	Leu	yrg	Arg	Ala	Val	qzA	Tyr	Leu	Ala	Gly	Gly	Ala	Ala	Leu		
					260					265					270			
				TTA														863
	Cys	Ser	Ala	Leu	Tyr	Vai	Gly	ązk		Cys	Gly	Ala	Leu		Leu	Val		
				275					290					285				
	GGC	САА	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAC	GCT	ACG	GTG	CAG	AAC		911
	Gly	Gla	Met	Phe	Thr	Tyr	Arg	Pro	yra	Gln	His	Ala	The	Val	Gln	Asr.		
			290					295					300					
				TCC													•	959
	CÀR		Cys	Ser	Ile	Tyr		Gly	His	Val	Thr	$G1\gamma$	His	Arg	Met	Ala		
		305					310					315						
	403																	
	(2)	TNEC	RMAT	IGN	FOR	SEQ	ID N	10: 5	i 0 :									
		(EQUE					-									
			-	LE					acid	!s								
			•-	3) TY 3) TO														
			1,2	, 10		· · ·		- A										

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

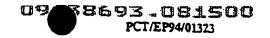
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asa Glu Gly Leu Gly Trp Ala Gly Trp 85 90



Leu Leu Ser	510	Arg	Gly	Ser	Arg	Pro	Asn	طتع	Gl~	220	Asn	Asp	Pro
	100				-	105		•	•		110		•

- Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys 115 120 125
- Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile 130 140
- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175
- Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
- Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro 195 200 205
- Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro 210 215 220
- Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val 225 230 235 240
- Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala 245 250 255
- Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys 260 265 270
- Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly 275 280 235
- Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys 290 295 300
- Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315
- (2) INFORMATION FOR SEQ ID NO: 51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:



(B) CLONE: PC-3-8

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

cc	ATG	AGC	ACG	AAT	ccT	***	CCT	ಜ ನ	AGA	AAA	ACC	AAA	AGA	AAC	ACC	47
	Mec	Ser	Thr	as:	SLO	Lys	PTO	Glm	Arg	Lys	Thr	Lys	۸rg	Asn	Thr	
	1		٠		5					10					15	•
AAC	: CG1	CGC	: cca	وجي	GAC	GTC	AAG	TTC	CCG	GGC	GGI	GGT	CAG	ATC	GTT	95
Ast	ı Arg	Arg	Pro	Gla	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	33
				20					25					30		
GGC	: GGP	GIT	TAC	TTG	TTG	ccs	CGC	AGG	GGC	CCI	AGG	ATG	GG:	GTG	CGC.	143
Gly	r Gly	Va!	TY	Leu	Leu	Pro	Arg	Arg	Gly	Pro	, Arg	Me:	Gly	Val	Arg	•
			35					40					45	i		
GCG	ACT	CGG	A AG	ACT	TCG	GAA	CGG	TCG	CAA	CCC	CGT	GGA	CGG	CGT	CAG	191
Ala	Thr			Thr	Ser	Glu			Gln	Pro	Arg	Gly	yra	Arg	Gln	
		50	,				55					60				
CCI	ATT	CCC	: AAG	GCG	CGC	CAG	CCC	ACG	GGC	CGG	TCC	TGG	GGT	ديب	. ccc	239
Pro	Ile 65		Lys	Ala	Yra		Sio	Thr	Gly	Arg		_	Gly	Gln	Pro	
						70					73					
GGG	TAC	CCI	. IGG	CCC	CII	TAC	GCC	AAT	GAG	GGC	CIC	GGG	TGG	GCA	GGG	257
6±7 80		Pro	LIP	Pro			Ala	Asn	Glu			Gly	Lin	Ala	Gly	
80					85					90					95	
TGG	CTG	CTC	TCC	CCT	CGA	GGC	TCT	ccc	CCT	AAT	TGG	GGC	ccc	AAT	GAC	335
<u>C</u> r1	Leu	Leu	Ser			Gīā	Ser	yrg	Pro	Asn	. Lib	Gly	Pro	Asn	czA.	
				100					105					110		
CCC	CGG	CGA	. AAA	TCG	CGT	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	383
															Thr	
			115					120					125			
TGC	GGA	TTC	GCC	GAT	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	ccc	431
Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	Pro	
		130					135					140				
															GAG	479
Val			Val	Ala	yra		Leu	Ala	His	Gly		-	Val	Leu	Glu	
	145					150					155				•	•
															TCT	527
		Val	Asn	Tyr			Gly	Asn	Leu			Cys	Ser	Phe		
160					165					170					175	
ATC	TIT	ATT	CTT	GCT	CTT	CTC	TCG	-TG:	CTG	ACC	GTT	CCG	GCC	TCT	GCA	575
Ile	Phe	Ile	Leu			Leu	Ser	Cys		Thr	Val	Pro	Ala		Ala	
				180					185					190		
GTT	ccc	TAC	CGA	AAT	GCC	тст	GGG	ATT	TAT	CAT	GTT	ACC	AAT	GAT	TGC	623

												-				
Val	Pro	Tyr	Azg 195	Asn	Ala	Ser	Gly	Ile 200	ī'n	His	Val	Thr	Asn 205	Asp	Cys	
Pro	AAC Asn	TCT Ser 210	TCC Ser	ATA Ile	GTC Val	TAT Tyr	GAG Glu 215	GCX Ala	GAT Asp	AAC Asn	CTG Leu	ATC Ile 220	CTA Leu	CAC His	GCA Ala	671
CCT Pro	GGT Gly 225	TGC Cys	GTG Val	CCT Pro	IGT Cys	GTC Val 230	ATG Mes	ACA Thr	GGT Gly	AAT Asn	GTG Val 235	AGT	AGA Arg	TGC Cys	TGG Trp	719
GTC Val 240	Gln	ATT Ile	acc The	cet Pro	ACA Thr 245	CTG Leu	TCA Ser	GCC Ala	CCG Pro	AGC Ser 250	CTC	GGA Gly	GCA Ala	GTC Val	ACG Thr 255	767
GCT Ala	CCT Pro	CTT	CGG Arg	AGA Arg 260	GCC Ala	GTT Val	GAC Asp	TAC Tyr	CTA Leu 265	GCG Ala	GGA Gly	GGG Gly	GCT Ala	GCC Ala 270	CTC Leu	815
TGC Cys	TCC Ser	GCG Ala	TTA Leu 275	TAC Tyr	GTA Val	GGA Gly	GAC Asp	GCG Ala 280	TGT Cys	GGG GGG	GCA Ala	CTA Leu	TTC Phe 285	TTG Leu	GTA Val	863
GGC	CAA Gla	ATG Mes 290	TTC Phe	ACC Thr	TAT Tyr	لاعك	CCT Pro 295	CGC	CAG Gln	CAC His	GCT Ala	ACG Thr 300	GTG	CAG Gln	AAC Asn	911
TGC Cys	AAC Asn 305	TGT Cys	TCC Ser	ATT Ile	TAC Tyr	AGT	GGC	CAT Kis	GTT Val	Thr	GGC Gly 315	CAC	SGS CGG	ATG Met	GCA Ala	959

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

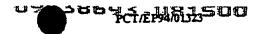
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60 - - - -

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80

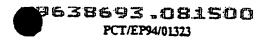


Tyr Pro Trp	Pro Leu	Ty	λla	Asa	Glu	Gly	Leu	Gly	T	Ala	Gly	Trp
	85					90					95	

- Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
- Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys 115 120 125
- Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val 130 140
- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 153 160
- Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175
- Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val 180 185 190
- Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
- Asm Ser Ser Ile Val Tyr Glu Ala Asp Asm Leu Ile Leu His Ala Pro 210 215 220
- Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val 225 230 235 240
- Gin The Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
- Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys 260 265 270
- Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly 275 280 285
- Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys 290 295 300
- Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC C/E1

(ix) FEATURE:

(A) NAME/NEY: CES

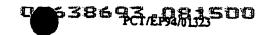
(B) LOCATION: 2..959

(xi) SEQUENCE DESCRIPTION: SEQ ID MC: 53:

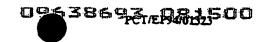
CCATGAGCA	GAATCCTAAA	CCTCLAAGAL	AAACCAAAG	AAACACCAAC	CGTCGCCCAC	60
AGGACGTCA	A GTTCCCGGGC	: GGTGGTCAGA	TCGTTGGCGG	AGTTTACTTG	TTGCCGCGCA	120
GGGGCCCTAC	GATGGGTGTG	CGCGCGACTC	GGAAGACTTC	GGAACGGTCG	CAACCCCGTG -	130
GACGGCGTC	GCCTATTCCC	AAGGCGCGCC	AGCCCACGGG	CCGGTCCTGG	GGTCAACCCG	240
GGTACCCTTC	GCCCCTTTAC	GCCAATGAGG	GCCTCGGTG	GGCAGGGTGG	CTGCTCTCCC	300
CTCGAGGCTC	TOGGCOTART	TGGGGCCCCA	ATGACTCCCG	GCGAAAATCG	CGTAATTTGG	360
GTAAGGTCAT	CGATACCCTA	ACGTGCGGAT	TCGCCCATCT	CATGGGGTAY	ATCCCGCTCG	426
TAGGCGGCCC	CRTTGGGGGC	GTCSCAAGGG	CTCTCGCACA	CGGTGTGAGG	GTCCTTGAGG	480
ACGGGGTAAA	CTATSCAACA	GGGAATTTAC	CCGGTTGCTC	TTTCTCTATC	TTTATTCTTG	540
CTCTTCTCTC	GTGTCTGACC	GTTCCGGCCT	CTGCAGTTCC	CTACCGAAAT	GCCTCTGGGA	600
TTTATCATGT	TACCAATGAT	TGCCCAAACT	CTTCCATAGT	CTATGAGGCA	GATAACCTGA	650
TCCTACACGC	ACCTGGTTGC	GTGCCTTGTS	TCATGACAGG	TAATGTGAGT	AGATGCTGGG	720
TCCAAATTAC	CCCTACACTG	TCAGCCCCGA	GCCTCGGAGC	AGTCACGGCT	CCTCTTCGGA	780
GAGCCGTTGA	CTACCTAGCG	GGAGGGGCTG	CCCTCTGCTC	CGCGTTATAC	GTAGGAGACG	840
CGTGTGGGGC	ACTATTCTTG	GTAGGCCAAA	TGTTCACCTA	TAGGCCTCGC	CAGCACGCTA	900
CGGTGCAGAA	CTGCAACTGT	TOCATTTACA	GTGGCCATGT	TACCGGCCAC	CGGATGGCA	959
10)						

- (2) INFORMATION FOR SEQ ID NO: 54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15



- Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30
- Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45
- Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
- Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80
- Tyr Pro Trp Pro Leu Tyr Ala Asm Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95
- Leu Leu Ser Pro Arg Gly Ser Arg Pro Asa Trp Gly Pro Asa Asp Pro
- Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
- Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val 130 135 140
- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 150 155 160
- Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175
- Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
- Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro 195 200 205
- Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro 210 215 220
- Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val 225 230 235 240
- Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala 245 250 255
- Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270
- Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly 275 280 285
- Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys 290 295 300
- Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315



(2)	INFORMATION	FCR	SEO	ID	NO:	55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANCEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CENA
- (iii) EYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-37

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

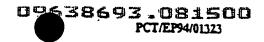
ACCACCGGAG	CTTCTATCAC	YIYCIICYCI	TACGGCAAGT	TCCTTGCTGA	TGGAGGGTGT	60
TCAGGCGGCG	CGCATGACGT	GATCATATGC	GACGAGTGCC	ATTCCCAGGA	CGCCACCACC	120
ATTCTTGGGA	TAGGCACTGT	CCTTGACCAG	GCAGAGACGG	CTGGAGCTAG	GCTCGTCGTC	190
TTGGCCACGG	NCACCCCTCC	CSGCAGTGTS	ACAACGCCCC	ACCCCAACAT	CGAGGAAGTG	240
GCCCTGCCTC	AGGAGGGGGA	GGTTCCCTTC	TACGGCAGAG	CCATTCCCCT	TGCTTTTATA	300
AAGGGTGGTA	GGCATCTCAT	CTTCTGCCAT	TCCAAGAAAA	ATTGTGATGA	ACTC	354

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala 1 5 10 15

Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val Ile Ile Cys Asp Glu 20 25 30



Cys	His	Ser	Gla	Asp	aلة	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	Val	Leu
		35					40					45			

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa 50 55 60

The Pro Pro Gly Ser Val The The Pro His Pro Ash Ile Glu Glu Val

Ala Leu Pro Gin Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys

Lys Asn Cys Asp Glu Leu 115

- (2) INFORMATION FOR SEQ ID NO: 57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cONA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE: (B) CLONE: PC-1-48
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..354
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT 60

TCAGGCGGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC 120

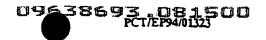
ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC 180

TTGGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGAAGTG 240

GCCCTGCCTC AGGAGGGGGA GGTTCCCTTC TACGGNAGAG CCATTCCCCT TGCTTTTATA 300

AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA AATGTGATGA ACTT 354

- (2) INFORMATION FOR SEQ ID NO: 58:
 - (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

The The Gly Ala Ser Ile The Tyr Ser The Tyr Gly Lys Phe Leu Ala
1 5 10 15

Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu 20 25 30

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu 35 40 45

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa 50 55 60

The Pro Pro Gly Ser Val The The Pro His Pro Asm Ile Glu Glu Val 65 70 75 80

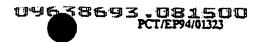
Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro 85 90 95

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys 100 105 110

Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu 115 120 125

Arg Pro Trp Glu Tyr 130

- (2) INFORMATION FOR SEQ ID NO: 59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SCURCE:
 (B) CLONE: PC-1-37
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS



(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ATGGCTTTCA	TGTCTCCGGA	CTTSGAGGTC	ATTACCANCA	CTTGGGTTCT	GGTGGGGGGC	60
GTTGTGGCSA	CCCTGNCGNC	CTACTGCTTG	ACGGTGGGTT	CGGTAGCCAT	AGTEGGTAGG	120
ATCATCCTCT	CTGGGAAACC	TGCCATCATT	NCCGATAGGG	AGGTATTATA	CCAGCAATTT	190
GATGAGATGG	AGGAGTGCTC	GGCCTCGTTG	CCCTATATGG	ACGARACACG	TNCCATTGCC	240
GGACAATTCA	AAGAGAAAGT	GCTCGGCTTC	ATCAGCACGA	CCGGCCAGAA	GGCTGAAACT	300
CTGAAGCCGG	CAGCCACGTC	TGTGTGGAAC	AAGGCTGATC	AGTTCTGGNC	CACATAC	357

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Ala Phe Met Ser Pro Asp Leu Glu Val Ile Thr Xaa Thr Trp Val 1 5 10 15

Leu Val Gly Val Val Ala Thr Leu Xaa Xaa Tyr Cys Leu Thr Val 20 25 30

Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala 35 40 45

Ile Ile Xaa Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu 50 55 60

Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Xaa Ile Ala 65 70 75 8J

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln 85 90 95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala 100 105 110

Asp Gln Phe Trp Xaa Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln 115 120 125

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

120

130

240

300

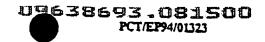
357

(A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPCLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NC
(Vii) IMMEDIATE SOURCE: (B) CLONE: PC-1-48
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1357
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:
ATGGCTTGCA TGTCTGCGGA CCTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGGC
GTTGTGGCGN CCCTGGCGGC CTACTGCTTG ACGGTGGGTT CGGTAGCCAT AGTCGGTAGG
ATCATCOTOT CTGGGAAACO TGCCATCATT CCCGATAGGG AGGCATTATA CCANCAATTT
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCCTATATGG ACGAGACACG TGCCATTGCC
GGACAATTCA AAGAGAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGANC AGTTCTGGGC CACATAC
(2) INFORMATION FOR SEQ ID NO: 62:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPCLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:
Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Va 1 5 10 15
Leu Val Gly Gly Val Val Ala Xaa Leu Ala Ala Tyr Cys Leu Thr Va 20 25 30
Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Al

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55

Ile Ile Pro Asp Arg Glu Ala Leu Tyr Xaa Gln Phe Asp Glu Met Glu



Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala 65 70 75 80

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln 85 90 95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala 100 105 110

Xaa Gln Phe Trp Ala Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln 115 120 125

- (2) INFORMATION FOR SEQ ID NO: 63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr161"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCCTCC

28

- (2) INFORMATION FOR SEQ ID NO: 64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP:162"

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:
GGGCTGCTCT ATCCTCATCG ACGCCATC
 (2) INFORMATION FOR SEQ ID NO: 65:
      (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 28 base pairs
           (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
   (iii) HYPOTHETICAL: YES
   (iii) ANTI-SENSE: NO
    (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 1..28
          (D) OTHER INFORMATION: /standard_name= "HCV Primer
                 HCPr163*
    (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 65:
GCCAGAGGCT CGGAAGGCGA TCAGCGCT
                                                                       28
(2) INFORMATION FOR SEQ ID NO: 66:
     (1) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 28 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: DNA (genomic)
  (iii) HYPOTHETICAL: YES
  (iii) ANTI-SENSE: YES
   (ix) FEATURE:
         (A) NAME/KEY: misc_feature
         (B) LOCATION: 1..28
         (D) OTHER INFORMATION: /standard_name= *HCV Primer
                HCPT164"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCCTCCTCG ACGCCGCA

Constant of the second of the second of the second

(2) INFORMATION FOR SEQ ID NO: 67:

28

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genemic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_mame= "HCV Primer HCPr23"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

- (2) INFORMATION FOR SEQ ID NO: 68:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP=54"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCAG TTCATCATCA TATCCCA

27

- (2) INFORMATION FOR SEQ ID NO: 69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

क्षा करणा विकास के किया है है। इस के किया के क्षेत्र के किया के किया के किया है कि किया है कि किया है कि किया क

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WO 94/25601
    (iii) HYPOTHETICAL: YES
    (iii) ANTI-SENSE: NO
    (ix) FEATURE:
           (A) NAME/KEY: misc_feature
           (B) LOCATION: 1..28
           (D) OTHER INFORMATION: /standard_name= "HCV Primer
                  HCPrl16.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:
 TITTAAATAC ATCATGRCTG YATG
 (2) INFORMATION FOR SEQ ID NO: 70:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 33 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (iii) HYPOTHETICAL: YES
    (iii) ANTI-SENSE: YES
```

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCCRCTGA TGAARTTCCA CAT

33

24

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

المساسدة المداوية والمحصارية فالسهاميسيسية بمساحيات المال الأداء المريد مساه فالطبية الأداء

(A) NAME/KEY: misc_feature



- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrl18:
- (x1) SEQUENCE DESCRIPTION: SEQ. ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

- (2) INFORMATION FOR SEQ ID NO: 72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (E) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrll7:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TITTAAATAC ATCGCRCTGC ATGCA

25

- (2) INFORMATION FOR SEQ ID NO: 73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP=119:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTOGAC TARTTGCATA GCCKRTTCAT CCAYTG

36

- (2) INFORMATION FOR SEQ ID NO: 74:(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 base pairs
 - (B) TYPS: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr131:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGGA ARTG

34

- (2) INFORMATION FOR SEQ ID NO: 75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= *HCV Primer HCPrl30:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

- (2) INFORMATION FOR SEQ ID NO: 76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (gen mic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= *HCV Primer HCPr134:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

2-3

- (2) INFORMATION FOR SEQ ID NO: 77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr3:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

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16 .

- (2) INFORMATION FOR SEQ ID NO: 78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - '(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: YES
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /scandard_name= *HCV Primer HC2r4:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

- (2) INFORMATION FOR SEQ ID NO: 79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (3) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP:152:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCCTCTT CTATATCGGT TGGGGCCTG

29

- (2) INFORMATION FOR SEQ ID NO: 80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrs2:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCATCGA TACCCT

26

- (2) INFORMATION FOR SEQ ID NO: 81:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr41:
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCGGGAGGT CTCGTAGACC GTGCA

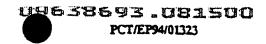
25

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- (2) INFORMATION FOR SEQ ID NO: 82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr40:



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(xi) SEQUENCE DESCRIPTION; SEQ ID NO: 82:

CTATTAAAGA TAGAGAAAGA GCAACCGGG

29

- (I) INFORMATION FOR SEQ ID NO: 83:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 192 to 203 of the V1 region of HCV type 3 $\,$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83: Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 84:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 85:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single



- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 213 to 223 of the V2 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val Tyr Glu Ala Asp Asp Val Ile Leu His Thr

- (2) INFORMATION FOR SEQ ID NO: 86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:

 (B) MAP POSITION: positions 213 to 233 of the V2 region of HCV type 5
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

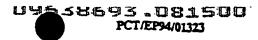
Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 87:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO

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(viii) POSITION IN PROTEIN:
(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV type 3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val

- (2) INFORMATION FOR SEQ ID NO: 88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met. Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile

- (2) INFORMATION FOR SEQ ID NO: 89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 248 to 257 of the V4 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 90:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 248 t 257 of the V4 region of HC/

type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala Pro Ser Leu Gly Ala Val Thr Ala Pro 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 294 to 303 of the V5 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg Pro Arg Arg His Gla Thr Val Gla Thr
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:

 (B) MAP POSITION: positions 294 to 303 of the V5 region of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Arg Pro Arg Gln His Ala Thr Val Gln Asn

- (2) INFORMATION FOR SEQ ID NO: 93:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
 - (B) MAP POSITION: positions 70 to 78 of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Trp Gly Gln 1 5

- (2) INFORMATION FOR SEQ ID NO: 94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTY: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR33 and BR36
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr 1 5

- (2) INFORMATION FOR SEQ ID NO: 95:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single



- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISCLATE: HD10
- (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 230 to 237 of the V3 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala

- (2) INFORMATION FOR SEQ ID NO: 96:
 - (i) SZOUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR36
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 248 to 257 of the V4 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser

- (2) INFORMATION FOR SEQ ID NO: 97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR36

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(viii) POSITION IN GENOME:
(B) MAP POSITION: Positions 1688 to 1707 of HCV type 3
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu Val Leu Tyr Gin
15

Gln Tyr Asp Glu 20

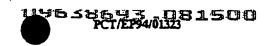
- (2) INFORMATION FOR SEQ ID NO: 98:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HD10
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1688 to 1707 of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Leu Gly Gly Lys Pro Ala Leu Val Pro Asp Lys Glu Val Leu Tyr Gln
1 10 15

Gln Tyr Asp Glu

- (2) INFORMATION FOR SEQ ID NO: 99:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1712 to 1731
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

.



Ser Gln Ala Ala Pro Tyr Il Glu Gln Ala Gln Val Ile Ala His Gln l 5 10 15

Phe Lys Glu Lys

- (2) INFORMATION FOR SEQ ID NO: 100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LZNGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR36
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1724 to 1743 of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala

1 5 10 15

Thr Gln Gln Gln 20

- (2) INFORMATION FOR SEQ ID NO: 101: (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HD10
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1724 to 1743 of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gin Phe Lys Glu Lys Ile Leu Gly Leu Leu Gin Arg Ala
1 10 15

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Thr Gln Gln Gln

- (2) INFORMATION FOR SEQ ID NO: 102:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANCEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: pepcide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENCME:
 - (B) MAP POSITION: positions 1688 to 1707 of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln
1 10 15

Gla Phe Asp Glu 20

- (2) INFORMATION FOR SEQ ID NO: 103:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1688 to 1707
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu

- (2) INFORMATION FOR SEQ ID NO: 104:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: position 1712 to 1731 of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln
1 5 10 15

Phe Lys Glu Lys

- (2) INFORMATION FOR SEQ ID NO: 105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1724 to 1743 of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile Ala Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr 1 5 10 15

Gly Gln Lys Ala 20

- (2) INFORMATION FOR SEQ ID NO: 106:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO



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	(B)	CLONE		GR4	Α.	٦.	חר

(ix) FEATORE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTC TAT Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr 1 5 10 15	46
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GCA ATT ACC GCC CTA Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu 20 25 30	94
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asm Ser Lys Gly Asp 	142
CTG TGC GGG TAT CGC AGA TGT CGC GCA AGC GGC GTC TAC ACC ACC AGC Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser 50 55	_ 190
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AAA Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys 65 70 75	238
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95	286
GTT GTC ATC GCT GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA CCC CTC Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu 100 105 110	334
GGA GCC Gly Ala	340

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln 1 5 15



Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala L u Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Mec His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys Ala 65 70 75 80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu Gly
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 108:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:

(B) CLONE: GB116-3-5

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:
- C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTA TAT 46
 Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr
 1 5 10 15
- CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AGA GCA ATT ACC GCC CTA

 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu

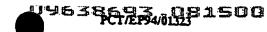
 20 25 30
- ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AGG GGA GAC

 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp

 35

 40

 45



CTG Leu	TGC Cys	GGG Gly	TAT Tyr	CGC Arg	AGA Arg	TGC Cys	CGT Arq	GCG Ala	AGC Ser	GGC Glv	GTC Val	TAC	ACC	ACC	AGC	190
		50			•		55			1	•	60	•••	****	361	
TTC	GGG	AAC	ACA	CTG	ACG	TGC	TAT	CTC	AAA	GCC	TCA	GCC	GCT	ATC	AGA	238
Phe	GTA	Asn	The	Leu	Thr	Cys	Ty:	Leu	Lys	Ala	Ser	Ala	Ala	Ile	Arg	230
	65					70					75					
GCG	GCG	GGG	CTG	AGA	GAC	TGC	ACC	ATG	TTG	GTC	TGT	CCT	GIT	GBC	CTC	286
ALA	Ala	Gly	Leu	کتع	Asp	Cys	Thr	Me:	Leu	Val	C'/S	Gly	Asp	Asp	Leu	200
80					85					90		•		,	95	
GTC	GTC	ATT	GCT	GAA	AGC	GAT	GGC	GTA	GAG	GZG	GZC	222	CGS	ccc	CT C	334
Val	Val	Ile	Ala	Glu	Ser	çzA	Gly	Val	Glu	Glu	Asp	Lvs	Ara	A?a	LAU	334
				100		-	·		105			-,-	,	110	200	
GGA	GCC															140
Gly	Ala															340

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu Thr

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 110:

		(A) I	ENGI	H: 3	40 b	ase	pair	·s							
		(3) 1	YPE:	nuc	leic	aci	d								
		{	C) S	TRAN	DEDN	ESS:	sin	gle								
				OPOL				•								
	(ii) мо	LECT	LE T	YPE:	CDN	Ά				•					
	(iii) HY	POTH	ETIC	AL:	NO										
	(iii) AN	TI-S	ense	: NO											
	(vii			ate Lone	-		3-8									
	(ix		ATUR													
		_		ame/: Ocat										•		•
		·														
	(xi	SE	OIEN	CE D	ECUS.	T DTT	ON.	ern	TD 37	0. 1						
C T	CC A	CI G	TA A	CC G	AA A	AA G	AC A	TC A	GG G	TC G	AG G	AG G	AG G	TA T	AT (46
S	er Ti 1	nr V	al T	hr G		As y	sp I	le A			lu G	lu G	lu V		-	
	•				5				,	10					15	
CAG	TGT	TGT	GAC	CTG	GAG	CCC	GAA	GCC	CGC	AAG	GTA	ATT	ACC	GCC	СТА	94
Gln	Cys	Cys	ςzκ	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Thr	Ala	Leu	,,
				20					25	-				30		
ACA	GAG	aca.		TAT	GTG	GGC	GGT	CC=	3.70	~~	* * ~	366	• • •	663	636	
Thr	Glu	Ara	Leu	Tyr	Val	Glv	Glv	Pro	Mer	Bie	AA:	Sar	Lize	Gliv	Ban	142
		-	35	-24		:		40			A311	36-	45	GLY	vañ	
~~-																
CIG	TGC	GGG	TAT	CGC	AGA	TGC	CGC	GCA	AGC	GGC	GTC	TAC	ACC	YCC.	AGC	190
202	cys	50	-7-	Arg	Arg	Cys	55	Aid	ser	GLY	vai	60 TV2	TRY	Thr	Ser	
		• •					• • •					00				
TTC	GGG	AAC	ACA	CTG	ACG	TGC	TAT	CTC	AAA	GCC	TCA	GCC	GCC	ATC	AGG	238
Phe		Asn	Thr	Leu	Thr		Tyr	Leu	Lys	Ala	Ser	Ala	Ala	Ile	Arg	
	65					70					75					
GCG	TCA	GGG	CTG	AGA	GAC	TGC	ACT	ATG	CTG	GTC	TAT	GGT	GAC	GAC	CTG	296
Ala	Ser	Gly	Leu	Arg	Asp	Cys	Thr	Met	Leu	Val	Tyr	Gly	Asp	Asp	Leu	
80					85					90	•	-	-	-	95	
GTC	GTC	ATT	GCC	GAG	AGC	GAT	GGC	GTA	GAG	GAG	GAC	AAA	CGA	GCC	CTC	334
Val	Val	Ile	Ala	Glu	Ser	Asp	Gly	Val	Glu	Glu	Asp	Lys	Arg	Ala	Leu	
				100					105		•	•	•	110		
GGA	GTC															340
	Val															340

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ser Thr. Val Thr Giu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Val

- (2) INFORMATION FOR SEQ ID NO: 112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (111) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB358-3-3
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:
- C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTG TAT



Ser Thr Val Thr	Glu Lys Asp Ile	a Arg Val Glu Glu G	lu Vai Tyr
1	5	10	15
C10 mom mom c10 cm	T 636 666 616 6		
		SCC CGC AAG GCA ATT	
		Ala Arg Lys Ala Ile	
4	10	25	30
ACA GAG AGA CTC TA	T GTG GGC GGT (DIC ATG CAT AAC AGC	AAG GGA GAC 142
		Pro Met His Asn Ser	-
. 35		40	45
CTG TGT GGG TAT CG	ic aga toc coc o	SCA AGC GGC GTC TAC	ACC ACC AGC 190
Leu Cys Gly Tyr Ar	g Arg Cys Arg J	Ala Ser Gly Val Tyr	Thr Thr Ser
50	55	. 60	
TTC GGG AAC ACA CT	G ACG TGC TAC (CTC AAA GCC TCA GCC	GCT ATC AGA 238
Phe Gly Asn Thr Le	u Thr Cys Tyr I	Leu Lys Ala Ser Ala	Ala Ile Arg
65	70	75	_
GCG GCG GGG CTG AG			
Ala Ala Gly Leu Ar		• •	• •
	85	90	95
GTC GTC ATC GCT GA	AG AGC GAT GGC O	STT GAG GAG GAC AAA	CGA GCC CTC 334
Val Val Ile Ala Gl			
10	• •	105	110
GGA GCC			340
Gly Ala			

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Glm 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr 20 25

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80



Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly

Ala

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB549-3-6
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

C TCC	ACG	GTG	ACC	GYY	AGG	GAT	ATC	AGG	ACC	GAG	GAA	GAG	ATC	TAC	4.6
Ser	Thr	Val	Thr	Glu	Arg	qzA	Ile	Arg	Thr	Glu	Glu	Glu	Ile	Tvr	10
1				5					10					15	

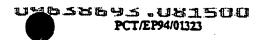
- CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA

 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu

 20
 25
 30
- ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp
 35
 40
 45
- CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC
 Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser
 50 55
- TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG
 Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg
 65
- GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA

 Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu

 80 85 90 95



GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC

Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu

100

105

110

CGA GCC Arg Ala

340

- (2) INFORMATION FOR SEQ ID NO: 115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gin
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser Phe 50 55 60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala 65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(vii)	IMMEDIATE SOURCE:	
	(B) CLONE: GB809-3-1	

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

C :	rcc : Ser :	ACT (FTG A	ACT G	AG A lu A S	rg y	AC A Sp I	TC A	iys V	TC G al G	AA o	iAA G ilu G	AA G Slu V	al T	AT Yr 15	46
CAC Glr	TG:	TGT Cys	GAT Asp	CTG Leu 20	GAG Glu	bro CCC	GAG Glu	GCC Ala	CGC Arg	Lys	GTA Val	ATA Ile	GCC Ala	GCC Ala 30	CTC Leu	94
	-	, mra	CTC Leu 35	TYT	AGT	Giy	GTÅ	Pro 40	Met	His	Asn	Ser	Lys 45	Gly	çek	142
CTT	TGC	GGG Gly 50	TAT	CGT Arg	AGA AIG	TGC Cys	CGC Arg 55	GCG Ala	AGC Ser	GGC	GTA Val	TAC Tyr 60	ACC Thr	ACC Thr	AGC Ser	190
TTC Phe	GGG Gly 65	AAC Asn	ACA Thr	ATG Met	ACG Thr	TGC Cys 70	TAC Tyr	CTT Leu	AAG Lys	GCC Ala	TCA Ser 75	GCA Ala	GCC Ala	ATC Ile	AGG Azg	238
GCT Ala 80	GCG Ala	GGG Gly	CTA Leu	AAG Lys	GAT Asp 85	TGC Cys	ACC Thr	ATG Met	CTG Leu	GTT Val 90	TGC Cys	GGT Gly	GAC Asp	GAC QeA	CTA Leu 95	286
GTC Val	GTG Val	ATC Ile	GCC Ala	GAG Glu 100	AGC Ser	GGT Gly	GGC Gly	GTT Val	GAG Glu 105	GAG Glu	GAC Asp	aaa Lys	Arg	GCC Ala 110	CTC Leu	334
GGA Glv					•											340

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln

1 5 10 15

179



Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 60

Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB358-4-1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG 96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

35

40

45



TCT	ATC Ile 50	TTC Phe	CTC Leu	TTG Leu	GCA Ala	CTT Leu SS	CTT	TCG Ser	TGC Cys	CTG Leu	ACT Thr 60	GTT Val	CCC	ACC Thr	TCG Ser	192
GCC Ala 65	Val	AAC Asn	TAT Tyr	CGC	AAT ASD 70	GCC Ala	TCG Ser	GGC Gly	ATC Ile	TAT Tyr 75	CAC His	ATC Ile	ACC Thr	AAT Asn	GAC Asp 80	240
TGC Cys	CCG Pro.	AAC Asa	TCG Ser	AGC Ser 85	ATA Ile	GTG Val	TAC Tyr	GAG Glu	ACC Thr 90	GAG Glu	CAC His	CAC His	ATC Ile	CTA Leu 95	CAC His	288
CTC	CCX Pro	GGG	TGT Cys 100	TTA Leu	PT0	TGC Cys	GTG Val	AGG Arg 105	GIT Val	GGG Gly	aat Asd	CAG Gln	TCA Ser 110	CGC	TGC Cys	336
TGG Trp	GTG Val	GCC Ala 115	CTC Leu	ACT Thr	CCC	ACC Thr	GTG Val 120	GCG Ala	GCG Ala	CCT Pro	TAC	ATC Ile 125	GGC Gly	GCT Ala	CCG Pro	384
CTT Leu	GAA Glu 130	TCC Ser	CTC Leu	CGG Arg	AGT Ser	CAT His 135	GTG Val	GAT Asp	CTG Leu	ATG Met	GTA Val 140	GGT Gly	GCC Ala	GCT Ala	ACT Thr	432
GCG Ala 145	TGC Cys	TCC Ser	GCT Ala	CTT Leu	TAC- Ty - 150	ATC Ile	GGA Gly	gac Qac	CTG Leu	TGC Cys 155	GGT Gly	GGC Gly	GTA Val	TTC Phe	TTG Leu 160	480
GTT Val	GGT Gly	CAG Gln	ATG Met	TTC Phe 165	TCT Ser	TTC Phe	CAG Gln	CCG	CGG Arg 170	CGC	CAC His	TCG Trp	ACT Thr	ACG Thr 175	CAG Gln	528
			TGT Cys 180												A	574

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asm Tyr Ala Thr Gly Asm Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser

50

55

60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His Hi Ile Leu His 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg 180 185 190

- (2) INFORMATION FOR SEQ ID NO: 120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE: (B) CLONE: GB549-4-3
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 10 15

CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG

Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

20

25

30

GTA	ĄSĄ	35	ATT Ile	Asn	Tyr	Ala	Thr 40	Gly	Asn	Leu	Pro	Gly 45	Сув	Ser	Phe		144
Ser	Ile 50	Phe	Leu	Leu	Ala	Leu 55	Leu	Ser	Cys	Leu	Thr 60	Val	Pro	Ala	Ser		192
65 A1a	Gln	His	TAC	Arg	70	Ile	Ser	Gly	Ile	75	His	Val	Thr	Asn	Asp 80		240
Cys	PTO	Asn	TCT Ser	Ser 85	Ile	Val	īřī	Glu	Ala 90	Asp	His	His	Ile	Met 95	His		288
CTA Leu	δżο CCY	GGG Gly	TGT Cys 100	GTG Val	CCT Pro	TGC Cys	GTG Val	AGA Arg 105	ACC Thr	GGG Gly	AAC Asn	ACC Thr	TCG Ser 110	CGC Arg	TGC Cys	•	336
Trp	GTT Val	CCT Pro 115	TTA Leu	ACA Thr	Pro	ACT Thr	GTG Val 120	GCT Ala	GCC Ala	CCC	TAT Tyr	GTT Val 125	GGC Gly	GCG Ala	CCG Pro		384
CTC	GAA Glu 130	TCC Ser	ATG Met	CGG Arg	CGG	CAC His 135	GTG Val	GAC Asp	TTA Leu	ATG Met	GTG Val 140	GGT Gly	GCC Ala	GCC Ala	ACC Thr	•	432
GTC Val 145	TGC Cys	TCG Ser	GCC Ala	CTG Leu	TAC Tyr 150	ATC Ile	GGA Gly	GAC QaA	CTT Leu	TGC Cys 155	GGA Gly	GGT Gly	GTC Val	TTC Phe	CTG Leu 160		480
GTC Val	GGG Gly	CAG Gln	ATG Met	TTC Phe 165	ACC Thr	TTC Phe	CGG Arg	CCG Pro	CGC Arg 170	CGC	CAT His	TTP TGG	ACT Thr	ACC Thr 175	CAG Gln		529
GAC Asp	TGC Cys	AAC Asn	TGC Cys 180	TCT Ser	ATC Ile	TAT Tyr	GAT Asp	GGC Gly 185	CAC His	ATC Ile	ACC Thr	GGC Gly	CAT His 190	AGA Arg	Α		574

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30



Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 153 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg 180 185 190

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE: (B) CLONE: GB809-4-3
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

49

Th	r Cy 1	rs G	Ly p	he i	Ala S	Asp	Leu	Me!	: Gly	7 Ty:	r Ile	Pr) Let	ı Va	l Gl ₃	/ Ala	
CC Pr	C GT O Va	T G(., •	GC (ly \ 20	JTC Val	GCC Ala	AGG Arg	GCS Ala	Leu 15	1 ALa	G CAT	GG(C GTO Y Val	AGG	, Ala	GTG Val	96
GA:	G GA 1 As		G A' Y I	IT ;	SAJ EaJ	<u>Làr</u> Lyi	GCG Ala	ACA Thi	GTA	AAT Ast	CTI Leu	Pro	GGT Gly 45	. CAS	TCI Se:	TTC Phe	144
TC:	T ATS		C CI	C C	TG æu	GCY YTS	CTT Leu 55	CTT	TCG Ser	TGC	CTC	ACT Thr	Val	Pro CCA	GCG Ala	TCA Ser	192
GCI Ala 63	GAC	CA Hi	C TA S Ty	.c c	ra ee	AAT Asn 70	GCT Ala	TCG Ser	GGC Gly	ATC Ile	TAT Tyr 75	CAC His	ATC	ACC Thr	TAA nea	GAC Asp 80	. 240
TGT Cys	bro CC0	AA :	T TC		GC er 85	GTA Val	GTC Val	TAT Tyr	GAA Glu	ACT Thr 90	GAC Asp	CAC	CAT His	ATA Ile	TTG Leu 95	CAC His	288
			10	0	-	FiJ	Cys	vai	Arg	Aia	Gly	Asn	Val	Ser	CGT Arg	Cys	, 336
,		115	y va.	- 4,		P.C	TILL	Vai 120	Ala	Ala	Val	Ser	Mec 125	ğ	GCT Ala	Pro	384
	130	-		- ~-	·y /	- 9	135	Vai	ÇZA	Leu	Me:	Val 140	Gly	Ala	GCC Ala	Thr	432
145	-,5	-	V 4.		1	50	va:	GΙΆ	Asp	Leu	Cys 155	Gly	Gly	Ala	TTC Phe	Leu 160	480
GTG Val	GGG Gly	CAG Gln	Met	Ph 16		icc :	Phe (CAG Gln	Pro	CGT Arg 170	CGC Arg	CAC His	TGG Trp	ACC Thr	ACG Thr 175	CAG Gln	529
GAT Asp	TGT Cys	TAA naA	TGC Cys 180	Se	C A T I	TC 1	rat i Pyr :	Thr	GGC (Gly) 185	CAT . His	ATC Ile	ACC Thr	Gly	CAC His 190	AGG Arg	A	574

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:



Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pr Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Ph 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125

Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg 180 185 190

- (2) INFORMATION FOR SEQ ID NO: 124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..31
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP:206"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGGGGATCCC GTATGATACC CGCTGCTTTG A

- (2) INFORMATION FOR SEQ ID NO: 125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: limear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HcPr207"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GGCGGAATTC CTGGTCATAG CCTCCGTGAA

30

31

- (2) INFORMATION FOR SEQ ID NO: 126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB358
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids(B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Gin His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Amino acid
 - (C) INDIVIDUAL ISOLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

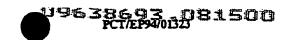
Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile 1 5 10

- (2) INFORMATION FOR SEC ID NO: 129:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISCLATE: GB358
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Tyr Glu Thr Glu His His Ile Leu His Leu 1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: pepcide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) CRGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:
- Val Tyr Glu Ala Asp His His Ile Met His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 131:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISCLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:
 - Val Tyr Glu Thr Asp His His Ile Leu His Leu 1 5 10
 - (2) INFORMATION FOR SEQ ID NO: 132:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB358



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 133:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SCURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 134:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val 1

- (2) INFORMATION FOR SEQ ID NO: 135:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino ficids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB358
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:
- Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:
 - Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 137:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:
 - Ala Val Ser Met Asp Ala Pro Leu Glu Ser 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MCLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISCLATE: GB358 and GB809
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Gln Pro Arg Arg His Tro Thr Thr Gln Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 139:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp 1

- (2) INFORMATION FOR SEQ ID NO: 141:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGGGATATGA TGATGAACTG GTC

23

- (2) INFORMATION FOR SEQ ID NO: 142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CCAGGTACAA CCGAACCAAT TGCC

24

- (2) INFORMATION FOR SEQ ID NO: 143:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE	TYPE:	CDNA
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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

																•
ATG	AGC	ACA	AAT	CCT	AAA	CCI	CXX	AGA	AAA	ACC	AAA	AGA	AAC	ACT	AAC	48
Met	Ser	The	Asn	Pro	Lys	Pro	Gla	Arg	Lys	The	Lys	yrg	Asn	Thr	Asn	•
1				5					10					15		
			G3.C	CZC	GTC	3 3 G	مائسك	CCG	GGC	GGT	GGC	CAG	ATC	GTT	GGT	96
CGC	CGC	CCA	CAG	DAC Den	Val	Lvs	Phe	Pro	Glv	Gly	Gly	Gla	Ile	Val	Gly	
AFG	Arg	P10	20	ر ده		-,-		25	•	•	•		30			
	•														000	144
GGA	GTA	TAC	TTG	TīG	CCG	CGC	AGG	GGC	222	CGG	TTG	GGT	GTG	CGC N-~	212	144
Gly	Val			Leu	bro	Arg	A25	GTÅ	ALO	AIG	Leu	45	vai	MEG	~	
		35					40									
ACG	AGG	AAA	ACT	TCC	GAG	CGG	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	192
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	yra	Gly	Arg	Arg	Gla	320	
	50					55					60					
						000	جے ہ	ccc	226	TCC	TGG	GGA	AAA	CCA	GGA	240
ATC	CCC	KAA	GAT	D.C.	Arc	Pro	Thr	Glv	Lvs	Sez	Trp	Gly	Lys	Pro	Gly	
116		Lys	MSP	~-3	70		•	,		75	•	_	•		80	
																288
TAC	CCT	TGG	CCC	CIG	TAC	GGG	AAT	GAG	GGC	CIC	GGC	TGC	GC	GGG	TGG	200
Tyr	Pro	Try	Pro			GJĀ	Asn	Glu	Gly 90	Leu	GTZ	TI) ATS	99	(III)	
				85	•				30	,			•			•
CTC	CTG	TCC		: CG	A GGG	TCT	CGC	CCG	TCA	TGG	GGG	: cc	A ACT	GA(2 000	336
Leu	Leu	Se	Pro	Arg	Gly	, Sez	Arg	Pro	se:	ııı	Gl	y PI	נתו כ	. AS) Pro	
			100					105	5				110)		
					~ 886	· •	: 661	7 220	GTO	ATC	: GA	T AC	C CT	r ac	G TGT	384
CGG	CAC	AGG	TC	- Are	z Asi	Lev	Gly	Lys	va!	Ile	a As	p Th	r Le	u Th	r Cys	;
Arg	nıs	11			,		120	,				12	5.			••
															3 GT	r 432
GG	TT	r gc	C GA	CCT	CAT	s GGG	TA	CAT	C CC.	r GTO	C GT	1 G1	. GC	a Pr	A GT	- L
Gl			a As	p Le	u me	2 G1)	y Ly: E	. 11	E FL	J 44.	14	0	,,		o Vai	
	130				•											
GG'	r GG	T GT	c GC	C AG	A GC	T CT	C GC	G CA	T GG	C GT	G AG	A G?	ד כז	G G	A GA	C 480
Gl	y Gl	y Va	1 Al	a Ar	g Al	a Le	u Al	a Hi	s Gl	y Va	l Az	g Va	il Le	u G1	u As 16	y
14		-			15	0				15	5				70	•

GG G1	G AT.	AAA RAS	C TAT	6 GC2 2 Ala 165	1111	GGG Gly	AAC AST	TTO Lev	Pro	GL	TG(Cys	TCC Ser	TT:	TCT Ser 175	ATC Ile		528
Phe	E TT	i Lei	GCC Ala 180	CTG Leu	CTA Leu	Ser	Cys	Ile 185	Th	' GTG	. Pro	GTC Val	TCC Ser	Gly	TTG Leu		576
		195		ACC Thr	342	ser	200	Tyr	Met	Val	Thr	205	Asp	Cys	Gln		624
AAC	AGT Ser 210		ATC	GTC Val	122 166	CAG Gln 215	CTC	AGG	GAT GAT	GCT Ala	GTT Val 220	Leu	CAC His	GTC Val	CCC Pro		672
GGG Gly 225	-,-	GTC Val	CCT	TGT Cys	GAG Glu 230	GAG Glu	AAG Lys	ej Å eec	AAC Asn	ATA Ile 235	TCC Ser	CGC Arg	TGT Cys	Tcc Trp	ATA Ile 240	•	720
CCG Pro	GTT Val	TCG Ser	Pro CCC	AAT Asn 245	ATA Ile	GCT Ala	GTG Val	AGC Ser	CAA Gln 250	CCT Pro	GGT Gly	GCG Ala	CTT Leu	ACC Thr 255	A AG Lys		768
GCC	CTG Leu	CGG Arg	ACG Thr 260	CAT His	ATT Ile	GAT Asp	ACC Thr	ATC Ile 265	ATT Ile	GCA Ala	TCC Ser	GCT Ala	ACG Thr 270	TIT Phe	TGC Cys	٠	816
TCT Ser	GCC Ala	CTG Leu 275	TAC Tyr	ATA Ile	GGA GLy	Asp	CTG Leu 280	TGT Cys	GGC Gly	GCG Ala	GTG Val	ATG Met 285	TTG Leu	GCT Ala	TCT Ser		864
~	GTC Val 290	TTC Phe	ATC Ile	ATC Ile	ser	CCC ?=o 295	CAG Gln	CAT His	CAT His	AAG Lys	TTT Phe 300	GTC Val	CAG Gln	GAC Asp	TGC Cys		912
AAC Asn 305	TGT Cys	TCC Ser	ATA Ile	TAC Tyr	Pro (GGC (Gly)	CAC	ATC Ile	Thr	GGA Gly 315	CAT His	CGG Arg	ATG Mec	GCG Ala			957

(2) INFORMATION FOR SEQ ID NO: 144:

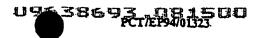
- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

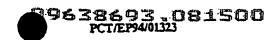


- Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45
- Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
- Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly 65 70 75 80
- Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95
- Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
- Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
- Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 150 155 160
- Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175
- Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu 180 185 190
- Gin Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gin 195 200 205
- Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro 210 215 220
- Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile 225 230 235 240
- Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys
- Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys 260 265 270
- Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser 275 280 285
- Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys
 290 295 300
- Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala 305 310 315
- (2) INFORMATION FOR SEQ ID NO: 145:
 - (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs



		(C) S	ype : Tran Opol	DEDM	ESS:	sin	_	•							
	(ii) MO	LECU.	LE T	YPE:	CDN	A									
	(iii) HY	POTH	ETIC	AL: 1	NO										
	(iii) an	TI-S	ense	: NO											
	(ix	()		e: Ame/I Ocat:				cide								
	(ix	(2		e : ame/1 ocat:			340					•		•		•
	(xi	SE(QUEN	CE DI	ESCR	ieti	วท : : :	SEQ :	ID N	0: 1:	45:					
C T	CA AG er Ti 1	og gr	rc ad	cg Gi	AG AG Lu Ai 5	ee e	AC AS	rc Ad le Ai	rg I'	CT G LT G 10	kg g lu g:	AG TO	er I	le T	ac Ye 15	4.6
CTT Leu	GCT Ala	TGC Cys	TCT Ser	TTA Leu 20	Pro CCC	GAG Glu	CAG Gln	GCA Ala	CGG Arg 25	ACT The	GCC Ala	ATA Ile	CAC His	TCA Sez 30	CTG Leu	94
ACT Thr	GAG Glu	AGG Arg	CTT Leu 35	TAC Tyr	GTG Val	GGA Gly	GGG Gly	CCC Pro 40	ATG Met	CTA Leu	Aac As::	AGC Ser	AAA Lys 45	GGG G1y	CAA Gln	142
				aga Arg												190
ATG Met	GGA Gly 65	AAT Asn	ACC Thr	ATC Ile	ACG Thr	TGC Cys 70	TAC Tyr	GTG Val	AAG Lys	GCA Ala	CAA Gln 75	GCA Ala	GCC Ala	TGT Cys	AAG Lys	238
				ATT Ile												286
				GAG Glu 100												334
CGA Arg																340

- (2) INFORMATION FOR SEQ ID NO: 146:
 - (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu 1 5 10 15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr

Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met 50 55 60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys Ala 65 70 75 80

Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asm Leu Arg 100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 147:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid

(D) TOPOLOGY: linear

- (C) STRANDEDNESS: single
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..345
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC



Met 1	Sez	Thr	Leu	Pro S	Lys	Pr	Gln	Arg	Lys 10	Thr	Lys	λrg	Asn	Thr 15	Asn		
510 CCC	GGC	CAC His	AGG Arg 20	ACG Thr	TTA Leu	AGT Ser	TCC Ser	CAG GLn 25	GCG Ala	GCG Ala	GTC Val	AGA Arg	Ser	TTG Leu	GTG Val		96
GAG Glu	T::	ACG Thr	TGC	TAC Tyr	CAC His	GCA Ala	GGG Gly	GCC	CCC	AGT Ser	TGG	GTG Val	30 TGC CVS	GTG Val	CAG		144
TGC	GCA	AGA	CII	CCG	AGC	GGT	40 CGC	ALC	CIC	GC3	GT3	45	ccc	336	663		• • • •
Суз	Ala 50	Arg	Leu	Pro	Ser	Gly 55	Arg	Asn	Leu	Ala	Val 60	Gly	Ala	Asn	Pro	•	192
TCC Ser 65	CCA Pro	GGG Gly	CGC Arg	GCC Ala	GAA Glu 70	Pro	AGG Arg	GCA Ala	GGT Gly	CCT Pro 75	GGG Gly	CTC Leu	AGC Ser	CCG Pro	GGT Gly 80		240
ACC Thr	CTT Leu	GGC Gly	CCC Pro	TAT Tyr 85	ATG Met	GGA Gly	ATG Met	AGG Arg	GCT Ala 90	GCG Ala	GGT Gly	GG Gly	CAG Gln	GGT Gly 95	G GC		288
TCC Ser	TGT Cys	Pro CCC	CGC Arg 100	GCG Ala	GCT Ala	CTC Leu	Ala	CGT Arg 105	CGT Arg	GGG Gly	GCC Ala	CAA Gln	ATG Met 110	ACC Thr	CCC Pro		336
Gly	Ala																345

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (3) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10

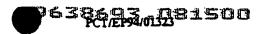
Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val

Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln

Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro

Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly 65 70 75 80

Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly



280

95

90	

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Glm Met Thr Pro 100 105 110

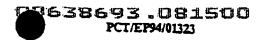
Gly Ala Gly

(2) INFORMATION FOR SEQ ID NO: 149:

85

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..280
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 2..277
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:
- G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC
 Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu
 1 5 10 15
- ACG GAG CGG CTT TAC TGT GGT GGT CCT ATG TTC AAC AGC AAG GGA CAA 94
 Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln
 20 25 30
- CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC
 His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser
 35 40 45
- TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA

 190
 Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys
 50
 60
- GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG 238
 Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu
 70 75
- GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG
 Val Val lle Ala Glu Ser Ala Gly lle Asp Glu Asp Arg Ala
 80 85 90
- (2) INFORMATION FOR SEQ ID NO: 150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids



- (B) TYPE: amino acid (D) TOPOLOGY: lin ar
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr

1 5 10 15

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe 35 40 45

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala 50 55 60

Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val 65 70 75 80

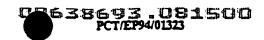
Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala 85 90

- (2) INFORMATION FOR SEQ ID NO: 151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..499
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (E) LOCATION: 1..496
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

1 5 10 15

CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGC
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30



		CCG PTO							144
		GAA Glu							192
		CAG Gln 70							240
		TAC Tyr							288
		GGC						•	336
		AAT Asn				 	 		384
		ATG Met			-	 	 	 •	432
		GCT Ala 150							480
	 TAT Tyr	 ACA Thr	G						499

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45



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Thr	Arg 50	Lys	Thr	Ser	Glu	Arg 55	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
Ile 65	Pro	Lys	Ala	Arg	Gla 70	PT	Thr	Gly	Arg	Ser 75	Trp	Gly	Gln	Pro	Gly 80	
Tyr	Pro	ţzp	Pro	Leu 85	ī'n	λia	Asc	Glu	Gly 90	Leu	Gly	Trp	Ala	Gly 95	Trp	
Leu	Leu	Ser	Pro 100	Arg	Gly	Ser	بد	Pro 105	Asn	îzp	Gly	Pro	Asn 110	Asp	Pro	
Arg	Arg	Lys 115	Ser	Arg	Asn	Leu	Gly 120	Lys	Val	Ile	Asp	Thr 125	Leu	Thr	Сув	
Gly	770					135					140					
Gly 145	Glγ	Val	Ala	Arg	Ala 150	Leu	Ala	His	Gly	Val 155	Arg	Val	Leu	Glu	As p 160	•
Gly	Val	Asn	īyr	Ala 165	Thr											
(2)	INFO	rmat	ION	FOR	SEQ	ID N	C: 1	.53 :								
		(A (B (C)) LE) TY) ST) TC	NGTH PE: RAND	ARAC :: 57 nucl EDNE GY:	9 ba eic SS: line	se p acid sing ar	airs	1							٠

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LCCATION: 1..576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC 48 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly 10

CCC GTT GGG GGC GTC GCA AGG GCT-CTC GCA CAC GGT GTG AGG GTC CTT Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu 20

GAG GAC GGG GTA AAC TAT. CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC



								-	•			-	_			
Glu	Asp	Gly 35	Val	Asn	IÀI	Pro	Thr 40	Gly	Asn	Leu	Pro	Gly 45	Cys	Ser	Phe	
				~~~			~~~	TCC	TGT	CTC:	200	GTT	CCG	GCC	TCT	192
ici	ATC	III	ATT	CTT	212	Tan	100	160	Cys	1.01	The	Val	Pro	Ala	Ser	
Ser		Phe	ITE	ren	wia		Leu	ser	Cys	744	60					
	50					55					•					
~~			#1 <i>C</i>	CG3	127	GCC		GGG	ATT	TAT	CRI	GII	ACC	AAT	GAT	240
٥٠٠	***	2	TAC	3	307	212	Ser	Glv	Ile	TV	His	Val	Thr	Asn	Aso	
65	val.	PES	ışı	λtg	70			4.,		75					80	
93					•											
TGC	CCA	220	شتك	TCC	ATA	GTC	TAT	GAG	GCA	GAT	عمد	CTG	ATC	CTA	CAC	298
Ove	Bro	Aen	Ser	Ser	Ile	Va1	TVI	Glu	Ala	Asp	Asa	Leu	Ile	Leu	His	
Cys	210	<i>-</i>		85			- 4 -		90	•				95		•
GCA	CCT	GGT	TGC	GTG	CCT	TGT	GTC	ATG	ACA	GGT	AAT	GTG	AGT	AGA	TGC	336
Ala	Pro	Glv	Cvs	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Val	Ser	Arg	Cys	
		,	100			•		105		_			110			
																•
TGG	GTC	CAA	ATT	ACC	CCT	ACA	CTG	TCA	GCC	CCG	AGC	C.C	GGA	GCA	GTC	384
Tro	Val	Gla	Ile	Thr	210	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	A_a	Val	•
-		115					120					125				
ACG	GCT	CCI	CTT	CGG	AGA	GCC	GII	GYC	TAC	CTA	GCG	GGA	GGG	GCT	GCC	432
Thr	Ala	220	Leu	Arg	Arg	Ala	Val	qzA	Tyr	Leu	λla	G'y	Gly	Ala	Ala	
	130					135					140					
																480
CTC	TGC	TCC	GCG	TTA	TAC	GTA	. GGA	GAC	GCG	TGT	GGG	GCA	. CIA	. TTC	TI	480
Leu	Cys	Ser	Ala	Leu			Gly	Asp	Ala			Ala	Leu	Pne	160	2
145					150	1				155					794	J
											- 636		- 300	: CT:	: (2)	523
GTA	GGC	: כא	ATG	TTC	: ACC	TAT	AGC	CCI	CGC	CAG			The	· Vai	61	~
Val	Gly	Gla	Met			Ty	. Are	, brc	Arg	GI	n.	, A=0		17		•
				165	,				170	,						
						י יייי י	. 200	r cer	CAI	سبت .	. 500	GGG	CAC	c ce	G AT	G 576
AAC	TGC	AAC	. rg:		. Ali	. LAG	. AU	- G1	/ His	. Vai	د توليات رجوده	- Glv	/ Hi!	s אביי	a Me	Ε
AST	Cys	ASI			. 116	. Ly:		189				,	190	0	•	
			180	,				10:	•							
																579
GCG																
Ala																

## (2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

PCT/EP94/01323

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

204

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 150 155 150

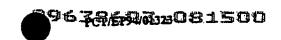
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met

Ala

# (2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO .
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..579
- (ix) FEATURE:
  - (A) NAME/KEY: mat_peptide
  - (B) LOCATION: 1..575



(xi) SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	155:	
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	,,							_									
ACG Thr 1	TGC Cys	GGA Gly	TTC Phe	GCC Ala S	<b>Y</b> ab CYC	CTC Leu	GTG Val	gjå eee	TAC Tyr 10	ATC Ile	310 CCG	CTC Leu	GTA Val	GGC Gly 15	GGC Gly	;	48
Pro	GTT Val	GGG Gly	GGC Gly 20	GTC Val	GCA Ala	AGG Arg	GCT Ala	CTC Leu 25	GCX Ala	CAT His	GGT Gly	GTG Val	AGG Arg 30	GTT Val	CT		96
GAG Glu	gac Asp	GGG Gly 35	GTG Val	AAT Asn	TAT Tyr	GCX Ala	ACA Thr 40	GGG Gly	AAT Asa	CTG Leu	CCT Pro	GGT Gly 45	TGC	TCT Ser	TT(	<b>c</b>	144
TCT Ser	ATC Ile 50	TTC Phe	ATT	CTT	GCA Ala	CTT Leu \$5	Leu	TCG Ser	TGC Cys	CTC Leu	ACT Thr 60	Val	CCG	GCC Ala	TC Se	<del>.</del>	192
GCA Ala 65	GTT Val	CCC Pro	TAC Tyr	CGA Arg	AAT Asn 70	Ala	TCT Ser	GGG G1y	ATC Ile	TAT Tyr 75	CAT His	GTC Val	ACC Thr	AAT Ass	. 22		240
TGC Cys	CCA Pro	OAA Sea	TCT Ser	TCC Ser 85	Ile	GTC Val	TAT Tyr	GLU	GCA Ala 90	ÇZÁ	GAT Asp	CTG Leu	ATC	CTA Lev 95	H	.c .s	288
GCA Ala	CCT	GGC Gly	TGC Cys	GTG	CCI Pro	TG1	GTG Val	AGG Arg	Lys	GAT Asp	AAT Ast	GTG Val	AGT Ser 110	AYS	TO F	iC /s	336.
TGG Trp	GTC Val	CA2 Glr	ı Ile	ACC Thi	. 650	ACC Thu	5 CTC r Lev 12	ı Se:	A GCC	CCG	AGG Se:	TTC Pho	s GT	A GCI	A GT a Va	IC al	384
ACC Thr	GCT Ala	Pro	CT.	r CG(	agi Ari	A GC: 3 Al. 13	a Va	T GA' l As	T TAC p Tyr	C TTC r Lev	GT( 1 Va. 14	1 G1	A GGG	G GC Y Al	T G	CC la	432
CTC Let	TGC	~ T/C	C GCC	G TT	A TA	r Va	T GG 1 Gl	A GA Y As	c GC p Al	G TG: a Cy: 15:	s Gl	g GC y Al	A CT a Le	A TI u Ph	e r	TG eu 60	480
~ <b>~</b>		c ca y Gl	A AT n Me	G TT c Ph 16	e Th	C TA	T AC	ig Pr	T CG	a er	G CA n Hi	T GC	T AC	G GT ir Va 17	IT G	AG Sla	528
GA:	c TG p Cy	C AA s As	C TG	T TC S Se	c AT	C TA	C AC	ST G0 er G1	y Hi	kC GT is Va	C AC	iz Gi	C CA Ly Hi	.s G.	AG A	NTG Met	576
GC Al																	579

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID BO: 156:

Thr. Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 20

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met

Ala

- (2) INFORMATION FOR SEQ ID NO: 157:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 530 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(iii)	HYPOTHETICAL:	NO
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(iii) ANTI-SENSE: NO

### (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..530

### (ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 3..527

### (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln 1 5 15	- 47
GTG GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GCT Val Val lie Asp lie lie Ala Gly Ser His Trp Gly Val Leu Phe Ala 20 25 30	<b>95</b>
GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val 35 40 45	143
TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly 50 55 60	191
TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC CGC GGC Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly 65 70 75	239
GCG CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATC Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile 80 85 90 95	297
AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile 100 105 110	335
GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp 115 120 125	383
CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly 130 135 140	431
ACT ATC AGC TAT GCC AAC ATA TCG GGT CCC AGT GAT GAC AAA CCA TAT Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr 145 150 155	479
TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG	527



Cys Trp His Tyr Pro Pro Arg Pr Cys Gly Val Val Pro Ala Gln Glu 160 165 170 175

GTC Val

530

- (2) INFORMATION FOR SEQ ID NO: 158:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 176 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val

Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala 20 25 30

Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu 35 40 45

Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser 50 55 60

Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala 65 70 75 80

Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn 85 90 95

Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala

Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg

Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr 130 135 140

Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys
145 150 155 160

Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val

- (2) INFORMATION FOR SEQ ID NO: 159:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

(D)	TOPOLOGY:	linear
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(ii) MOLECULE TYPE: cDNA

(iii) HYPCTHETICAL: NO

(iii) ANTI-SENSE: NO

#### (ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 2..340

### (ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..337

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr 1 5 10 15	46
CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu 20 25 30	. 94
ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA Thr Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln 35 40 45	142
CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACT ACT AGT Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser 50 60	190
ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg 65 70 75	238
GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu 80 85 90 95	286
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCA AGC CTG Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu 100 105 110	334
AGA GCC Arg Ala	340

### (2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln 1 5 10 15

Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr 20 25 30

Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met 50 55 60

Gly Asm Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala 65 70 75 80

Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg

Ala

- (2) INFORMATION FOR SEQ ID NO: 161:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 2..340
  - (ix) FEATURE:
    - (A) NAME/KEY: mat_peptide
    - (B) LOCATION: 2..337
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
- C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

	1				5					10					15		
CAA Gln	TCA Ser	TGT Cys	GAC Asp	TCG Ser 20	CAG Gln	Pro Pro	GAC Asp	GCA Ala	CGC Arg 25	GCA	GCA Ala	ATA Ile	CGG	TCA Ser 30	CTC Leu		94
AEC Thr	CXA Gl::	Arg	TTG Leu 35	TTC Phe	TGT Cys	GGA Gly	GGC Gly	CCC Pro 40	ATG Met	TAT Tyr	AAC Ase	AGC Ser	AAG Lys 45	GGG Gly	Caa Gl::	:	142
CAA Gla	TGT Cys	GGT Gly 50	TAT Tyr	Y.A CCC	AGA Arg	TGC Cys	CGC Arg 55	GCC Ala	AGC Ser	GGC Gly	GTC Val	TTC Phe 60	ACC Thr	ACC Thr	AGT Ser	:	L90
ATG Met	GGC Gly 65	AAC Asn	ACC Thr	ATG Met	ACG Thr	TGC Cys 70	TAC Tyr	ATT	AAG Lys	GCT Ala	TTA Leu 75	GCC Ala	TCC Ser	TGT Cys	AGA Arg	2	238
ACC Thr 80	GCT Ala	GGG Gly	CTC Leu	CGG Arg	GAC Asp 85	TAC Tyr	ACG Thr	CTC Leu	CTG Leu	GTG Val 90	TGT Cys	GGT Gly	GAC Asp	GAT Asp	CAT His 95	- 2	86
GTG Val	GCC Ala	ATC Ile	TGC Cys	GAG Glu 100	AGC Ser	CAG Glm	GGG Gly	ACA Thr	CAC His 105	GAG Glu	gar Gar	GAA Glu	GCG Ala	AAC Asn 110	CTG Leu		134
AGA Arg																3	40

# (2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

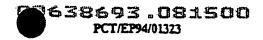
Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr Gln 1 5 10 15

Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu Thr
20 25 30
Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
35

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met

Gly Asn Thr Met Thr Cys Tyr Ile-Lys Ala Leu Ala Ser Cys Arg Thr
65 70 75 80

Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His Val



Ala	11	Càa	Glu	Ser	Gla	Gly	The	His	Glu	Asp	Glu	Ala	Asn	Leu	Ara
			100					105					110		

Ala

### (2) INFORMATION FOR SEQ ID NO: 153:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

#### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..499

### (ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..496

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ATG Met 1	AGC Ser	ACG Thr	TAA Asn	CCT Pro 5	AAA Lys	CTT	CAA Gln	AGA Arg	AAA Lys 10	ACC Thr	AAA Lys	CGT Arg	AAC Asn	ACC Thr 15	AAC Asn	48
CGC Arg	CGC	CCC Pro	ATG Met 20	GAC Asp	GTT Val	AAG Lys	TTC Phe	CCG Pro 25	GGT Gly	GGT Gly	GGC Gly	CAG Gln	ATC Ile 30	GTT Val	GGC Gly	96
GGA Gly	GTT Val	TAC Tyr 35	TTG Leu	TTG Leu	CCG Pro	Arg CGC	AGG Arg 40	GGC Gly	CCT Pro	AGG Arg	TTG Leu	GGT Gly 45	GTG Val	CGC	GCG Ala	144
ACT Thr	CGG Arg 50	AAG Lys	ACT Thr	TCG Ser	GAG Glu	CGG Arg 55	TCG Ser	CAA Gln	CCT Pro	CGT Arg	GGG Gly 60	AGG Arg	CGC	CAA Glm	CCT Pro	192
ATC Ile 65	Pro	AAG Lys	GCG Ala	CGC	CGA Arg 70	TCC Ser	GAG Glu	Gly	AGA Arg	TCC Ser 75	Trp	GCG Ala	CAG Gln	Pro CCC	GGG Gly 80	240
TAT	CCT Pro	TGG Trp	Pro CCC	CTT Leu 85	TAC Tyr	G27 G25	AAT Asn	-GAG Glu	GGC Gly 90	TGT Cys	GGG Gly	TGG Trp	GCA Ala	GGG Gly 95	TGG T:p	298
CTC	CTG	TCC	CCT	CGC	GGG	TCT	CGG	CCG	TCT	TGG	GGC	CCT	AAT	GAT	ccc	336



Leu	Leu	Ser	Pro 100	Arg	Gly	Ser	Arg	PT0 105	Ser	Trp	Gly	Pr	Asn 110	Asp	Pro		
					AAC Asn											384	Ł
					ATG Met											432	2
					GCC Ala 150											480	3
				GCA Ala 165	ACA Thr	G										499	₹

- (2) INFORMATION FOR SEQ ID NO: 164:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 166 amino acids
    - (3) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro

Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 - 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val 130 135 140



Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp 145 150 155 160

Gly Ile Asn Tyr Ala Thr 165

## (2) INFORMATION FOR SEQ ID NC: 155:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDMESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGAGCACGA	ATCCTAAACC	TCAAAGAAAA	ACCAAACSTA	ACACCAACCS	CCGCCCTATG	60
GACGTTAAGT	TCCCAGGCGG	TGGTCAGATC	GTTGGCGGAG	TTTACTTGTT	GCCGCGCAGG	120
GGCCCCAGGT	TGGGTGTGCG	CGCGACTCGG	AAGACTTCGG	AGCGGTCGCA	ACCTCGTGGG .	180
AGGCGCCAAC	CTATCCCCAA	GGCGCGCCGA	ACCGAGGGCA	GATCCTGGGC	GCAGCCCGGG	240
TATCCTTGGC	CCCTTTACGG	CAATGAGGGC	TGTGGGTGGG	CAGGGTGGCT	CCTGTCCCCT	300
CGCGGNTCTC	GGNCGTCTTG	GGGCCCCAAT	GATCCCCGGN	GGAGATCCCG	CAACTTGGGT	360
AAGGTCATCG	ATACCCTAAC	ATGCGGCTTC	GCCGACCTCA	TGGGATACAT	CCCGCTTGTA	420
GGCGCCCCG	TGGGTGGCGT	CGCCAGGGCC	CTGGCACATG	GTGTTAGGGC	TGTGGAAGAC	480
GGGATCAATT	ATGCAACAG					499

# (2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

144

30

WO 24/2580I		•	215		PCT/EP94/01	L323
1		5		10	15	
Arg A	rg Pro Met 20	Asp Val Lys	Phe Pro	Gly Gly Gly	Gln Ile Val Gly	
Gly V	al Tyr Leu 35	Leu Pro Arg	Arg Gly	Pro Arg Leu	Gly Val Arg Ala 45	
Thr A		Ser Glu Arg 55	Ser Gla	Pro Arg Gly 60	Arg Arg Glm Pro	
Ile P	ro Lys Ala	Arg Arg Thr 70	Glu Gly	Arg Ser Trp 75	Ala Gln Pro Gly 80	
Tyr P		Leu Tyr Gly 85		Gly Cys Gly 90	Trp Ala Gly Trp 95	
Leu L	eu Ser Pro 100	Arg Xaá Ser	Arg Xaa 105	Ser Trp Gly	Pro Asn Asp Pro-	
Arg X	aa Arg Ser 115	Arg Asn Leu	Gly Lys	Val Ile Asp	Thr Leu 125	
(2) INFORM	ATION FOR S	EQ ID NO: 1	67:			
	EQUENCE CHA (A) LENGTH: (B) TYPE: n (C) STRANDE (D) TOPOLOG	579 base p ucleic acid DNESS: sing	airs		·	
(ii) Mo	OLECULE TYP	E: cDNA				
(iii) H	YPOTHETICAL	: NO -				
(iii) A	NTI-SENSE:	NO				
	eature: (a) name/ke (b) locatio		·	·		
	EATURE: (A) NAME/KE (B) LOCATIO		ide			
(xi) SI	EQUENCE DES	CRIPTION: S	EQ ID NO:	167:		
				TC CCG CTT C		49

CCC GTG GGT GGC GTC GCC AGG GCC-CTG GCA CAT GGT GTT AGG GCT GTG

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CTT CCC GGT TGC TCC TTT

20



Glu	Asp	Gly 35	Ile	Asn	Ιγι	Ala	Thr 40	Gly	Asn	Leu	Pro	Gly 45	Суз	Ser	Phe	
TCT	ATC	TTC	CTC	TTG	GCG	CTC	CIC	TCG	TGC	Cre	۵۲۳	ملمئت	مانات	803	TCG	100
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Thr	Ser	192
	50					55			•		60				001	
GCC	GTT	AAC	727	CGC	222	GCT	TCG	GGC	ATT	TAT	CAC	ATC	ACC	AAT	GAC	240
Ala	Val	Asn	Tyr	Arg	Asn	Ala	Sez	Gly	Ile	Tyr	His	Ile	Thr	Asn	Aso	240
63					70					75					80	
TGC	CCG	AAT	GCA	AGC	ata	GTG	TAC	GAG	ACC	GAA	aat	CAC	ATC	TTA	CAC	288
Cys	Pro	Asn	Ala	Ser	Ile	Val	Tyr	Glu	Thr	Glu	Asn	His	Ile	Leu	His	
				85	٠				90					95		
CTC	CCA	GGG	TGC	GTA	CCC	TGT	GTG	AGG	ACT	GGG	AAC	CAG	TCG	CGG	TGT	336
Leu	Pro	Gly	Cys	Val	Pro	CA2	Val		Thr	Gly	Asn	Gln	Ser	Arg	Cys	
			100					105			:		110			•
TGG	GTG	GCC	CTC	ACT	CCC	ACA	GTA	GCG	TCG	CCA	TAC	GCC	GGT	GCT	CCG	384
ızb	Val	Ala	Leu	Thr	510	Thr	Val	Ala	Ser	Pro	Tyr	Ala	Gly	Ala	Pro	
		115					120					125				
CIT	GAG	CCC	TTG	CGG	CGT	CAT	GTG	GAC	CTG	ATG	GTA	GGT	GCT	GCC	ACC	432
Leu	Glu	Pro	Leu	Arg	Arg	His	Val	ςεA	Leu	Met	Val	Gly	λla	Ala	The	
	130					135					140					
ATG	TGT	TCC	GCC	CTÇ	TAC	ATC	GGC	GAC	TTG	TGC	GGT	GGC	TTA	TTC	TTG	480
Met	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	ζεK	Leu	Cys	Gly	Gly	Leu	Phe	Leu	
145					150					155					160	
GTG	GGC	CAA	ATG	TTC	ACC	TTC	حمم	CCG	CGA	CGT	CAC	TGG	ACC	ACT	CAG	528
Val	Gly	Gln	Met	Phe	Thr	Phe	Gln	Pro	Arg	Arg	His	<u>dt.</u>	Thr	Thr	Glm	
				165					170					175		
GAC	TGC	AAT	TGT	TCC	ATC	TAC	ACG	GGC	CAC	ATT	ACG	GGT	CAT	CGG	ATG	576
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	Bis	Ile	Thr	Gly	His	Arg	Met	
			180					185					190	,		
GCA																579
Ala																

### (2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15



Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys S r Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Pha Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

### (2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..579
- (ix) FEATURE:
  - (A) NAME/KEY: mat_peptide
  - (B) LOCATION: 1..576

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	169:
------	----------	--------------	-----	----	-----	------

AC	A TGC	. (23	- 7-74		. 636	. ~~~					_					
Thi	Cys	Gl ₃	/ Phe	Ala	Asp	Leu	Mes	GGA	TAC	ATC	CCC	; C	GTA	GGC	GCC	48
1				5					10		PIC	, rea	VAI	Giy 15		
ccc	GTC	: cc	· ccc	سجت ا												
Pro	Val	Glv	Glv	Val	Ala	AUA TT	GCC ala	CTG	GCA	CAC	GGT	GII	AGG	GCT	GTG Val	96
			20			~~3	~~~	25	Aid	HIS	GIY	' Val			Val	
													30			
GAA	GAC	GGG	ATC	AAC	TAC	GCA	ACA	GGG	AAT	CTC	ccc	GGT	TGC	TCC	TTT	144
GIN	Asç	35 GLY	TTE	Asn	Tyr	Ala	Thr	Gly	Asa	Leu	Pro	Gly	Cys	Ser	Phe	
							40				•	45				
TCT	ATC	TTC	CTC	TTG	GCA	CTT	CTC	TCG	TGC	CTC	ACT	سنت	-	c	TCG	
Ser	176	FRE	Leu	Leu	Ala	Lau	Leu	Ser	Cys	Leu	The	Val	Pro	Aia	Ser	192
	50					55					60					-
GGC	GTT	220	TAT	can	ልኔሞ	CCT	T									
Gly	Val	Asn	TAT Tyr	Ara	Asn	Ala	Ser	GGC	GTT Val	TAT	CAC	ATC	ACC	AAC	GAC	240
65				3	70			917	AGT	75	nıs	176	TRE	Asn	Asp 80	
TGC	CCG	AAT	GCG	AGC	ATA	GTG	TAC	GAG	ACC	GAC	AAT	CAC	ATC	TTA	CAC	. 288
cha	PIO	ASR	Ala	Ser 85	Ile	Val	IÀL	Glu	Thr	Asp	Asn	His	Ile	Leu	His	
				63					90					95		
CTC	CCA	GGG	TGC	GTA	CCC	TGT	GTG	AAG	ACC	GGG	AAC	CZG	TCG	CCG	TCT	336
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Lys	Thr	Gly	Asn	Glm	Ser	Arg	Cys	316
			100					105					110	•	•	
TGG	GTG	GCC	СТС	ACT	ccc	803	سخت	ccc								
Trp	Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Se~	Pro	TAC	GTC	GGT	GCT	CCG	384
		115					120				• } -	125	GLY	Aid	PIO	
Leu	GAG	550	TTG	CGG	CGC	CAT	GTG	GAC	CIG	ATG	GTA	GGT	GCT	GCC	ACC	432
	130		Leu	Arg	Arg	135	vai	ASD	Leu	Met		Gly	Ala	Ala	Thr	
						_					140					
GTG	TGC	TCC	GCC	CTC	TAC	GTC	GGC	GAC	CTG	TGC	GGT	GGC	TTA	TTC	TTG ·	480
Val 145	Cys	Ser	Ala	Leu	Tyr	Val	GĵÀ	Asp	Leu	Cys	Gly	Gly	Leu	Phe	Leu	•
743					150					155					160	
GTA	GGC	CAA	ATG	TTC	ACC	TTC	CAA	CCG	CGA	CGC	CAC	TGG	acc.	acc.	CNG	539
Val	Gly	Gln	Met	Phe	Thr	Phe	Gla	Pro	Azg	Arg	His	Lan	Thr	The	Gln	528
				165		•			170	_		•		175		
GAC	тст	דממ	ጥርም	ጥርር	ስጥ <u>ሮ</u>	T3.7	~~		<b>~</b> ~						•	
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ala	61v	CAT Hie	ATT Tla	ACG	GGC	CAT	CGG	ATG	576
-	-		180			-,-	- <b></b>	185		- + 5	4112		190	wig	MEC	
GCT Ala																579

(2) INFORMATION FOR SEQ ID NO: 170:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEO ID NO: 170:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala Ris Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 60

Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

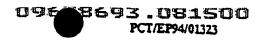
Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

- (2) INFORMATION FOR SEQ ID NO: 171:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA



(iii)	HYPOTHETICAL:	NO
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(iii) ANTI-SENSE: NO

### (ix) FEATURE:

(A) NAME/KEY: OS

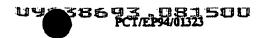
(B) LOCATION: 1..579

### (ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..576

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

								_		•	•••					
ACA Thr	Cys	GGC Gly	TTC Phe	GCC Ala 5	ASD	CTC	ATG Met	GGA Gly	TAC	Ile	Pro CCG	CTT Leu	GTG 'Val	GGC Gly	GCC Ala	48
CCT	GTT Val	GGT Gly	GGC Gly	GTC Val	GCC Ala	AGA Azg	GCC Ala	CTT Leu 25	λla	CAC His	GGC	GTC Val	Yzê	C	GTG Val	96
GAA Glu	GAC Asp	GGG Gly 35	ATT Ile	AAC Asn	TAT Tyr	GCA Ala	ACA Thr	GGG	AAC	CTT Leu	CCT Pro	Gly	TGC Cys	TCC Ser	TTT Phe	144
TCI Ser	ATC Ile 50	TTC	CTT Leu	CTG Leu	GCA Ala	CTT Leu 55	CIC	TCG Ser	TGC Cys	CTG Leu	Thr	45 GTC Val	CCC Pro	GCC Ala	TCG Ser	192
GCT Ala 65	GTG	CAT His	TAT Tyr	CAC His	Asn	ACC	TCG Ser	GGC Gly	ATC Ile	īķī	CAC His	CTC Leu	ACC Thr	AAT Asn	GAC Asp	240
TGC	CCT Pro	AAC Asn	TCT Ser	Ser	70 ATA Ile	GTC Val	TTT Phe	GAG Glu	GCX Ala	75 GTC Val	CAT His	CYC	ATC Ile	TTG Leu	CAC His	298
CTT Leu	CCA Pro	GGA Gly	TGC Cys	85 GTC Val	CCT Pro	TGT Cys	GTA Val	AGA Arg	90 ACT Thr	GGG Gly	AAC Asd	CAG Gln	TCT Ser	95 CGG Arg	TGC Cys	336
TGG	GTA	GCC	TTG Leu	ACC	CCC	ACG	CTG	105 GCC	GCG	CCA	TAC	CTT	110	GCT.	CCA	384
CTC	GAG	TCC	ATG	CGG	CGT	CAC	120 GTG	GAT	TTG	ATG	GTG	125 GGC	ACT	GCT.	ΔĊΔ	432
TTG	130 TGC	TCA	Met GCA	CTC	TAC	135 GTT	GGG	GAC	CTG	TGC	140 GGG	GGC	AT2	TTC	СТА	430
145 GCG	Cys GGC	Ser CAG	Ala ATG	Leu TTC	Tyr 150 ACC	Val TTC	CGG GJÀ	Asp	Leu	Cys 155 CTC	Gly	Gly	Ile	Phe	Leu 160 CAG	528
Ala	Gly	Gln	Met	Phe 165	Thr	Phe	Arg	Pro	Arg 170	Leu	His	Trp	Thr	Thr 175	Gln	J20



GAG			Thr						576
GCG Ala									579

- (2) INFORMATION FOR SEQ ID NO: 172:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu 145 150 155 160

Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln 165 170 175

Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

### (2) INFORMATION FOR SEQ ID NO: 173:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CONA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

#### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

#### (ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ACG	TGC	GGT	TCC	GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	СТС	GTA	GGC	GCC	48
1	cys	GIÀ	ser	Ala 5	ASD	Leu	Met	Gly	19 <u>2</u>	lie	Pro	Leu	Val	Gly 13	Ala	
CCT	GTG	GGT	GGC	GTC	GCC	AGG	GCC	TTG	GCG	CAT	GGC	GTC	AGG	GCT	GTG	96
Pro	Val	Gly	Gly 20	Val	Ala	Arg	Ala	Leu 25	Ala	His	Gly	Val	Arg 30	Ala	Val	
GλG	GAC	GGG	ATA	AAC	TAT	GCA	ACA	GGG	AAC	CTT	CCT	GGT	TGC	TCT	TTT	144
Glu	çaA	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
		35					40					45				
TCT	ATC	TTC	CIT	CTG	GCA	CTT	CTC	TCG	TGC	CTG	ACT	GTC	CCC	GCC	TCA	192
Ser	Ile	Phe	Leu	Leu	Ala		Leu	Ser	Ç'na	Leu		Val	Pro	Ala	Ser	
	50					55					60					
								GGC								240
	Val	His	Tyr	His	Asn	Thr	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp	
65					70					75					.80	
								GAG								298
Cys	Pro	Asn	Ser		Ile	Val	Phe	Glu	Ala	Glu	His	His	Ile	Leu	His	
				85					90					95		
CTT	CCA	GGA	TGC	GTC	ccc	TGT	GTG	AGA	ACT	GGG	AAC	CAG	TCA	CGA	TGC	336
								-yza								
			100					105					110			
TGG	ATA	GCC	TTG	ACC	CCT	ACG	TTG	GCC	GCG	CCA	CAC	ATT	GGC	GCT	CCA	384
								Ala								
													•			

115 120

CTT GAG TCC ATG CGA CGT CAT GTG GAT TTG ATG GTA GGC ACT GCC ACA 432 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr 130 135 TTG TGC TCC GCA CTC TAC ATT GGA GAT CTG TGC GGA GGC ATA TTT CTA 480 Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu GTG GGC CAG ATG TTC AAC TTC AGG CCC CGC CTG CAC TGG ACC ACC CAG 528 Val Gly Gln Met Phe Asm Phe Arg Pro Arg Leu His Trp Thr Thr Gln 170 GAG TGC AAT TGT TCC ATC TAT CCA GGC CAC ATC ACG GGT CAC AGA ATG 576 Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met 180 185 GCG 579 Ala

- (2) INFORMATION FOR SEQ ID NO: 174:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro 115 120 125

						•		22	4							
Let	130	Ser	Met	Arg	Arg	His 135	Val	Asp	Leu	Met	Val 140		Thr	Ala	Thr	
Let 145	Cys	Ser	Ala	Leu	Tyr 150	Ile	Gly	Asp	Leu	Суз 155	Gly	Gly	Ile	Phe	Leu 160	
				165	Asn				170					175		
Glu	Cys	Asn	180 Cys	Ser	Ile	ī'n	Pro	Gly 185	Zis	Ile	Thr	Gly	Ais 190	Arg	Met	
Ala	l															
(2)	INF	ORMA	TION	FOR	SEQ	ID 1	NO: :	175:								
	(±	(; (;	A) Li B) Ti C) Si	engti Pe : Trani	EARAC E: 57 nucl DEDNE DGY:	79 ba Leic ESS:	ase p acid	pairs i	3							-
	(ii)	MO	LECUI	LE T	PE:	CDNA	4									
	(111)	HY	POTH	TIC	L: N	O										•
	(iii)	AN.	FI-SI	ense:	. NO											
	(ix)	(2		ME/3	CEY:		579									
	(ix)	(2	ATURS A) NZ B) LO	ME/S	ŒY: :On:	mat_ 15	pept 176	ide								
					SCRI											
Thr 1	Cys	Gly	Phe	Ala 5	GAC Asp	Leu	Met	Gly	Tyr 10	Ile	Pro	Leu	Val	Gly 15	Ala	48
CCT Pro	GTG Val	ggt Gly	GGC Gly 20	GTC Val	GCC Ala	AGG Arg	GCC Ala	TTG Leu 25	GCA Ala	CAT His	GGT Gly	GTC Val	AGG Arg 30	GCC Ala	GTG Val	96
Glu	Asp	Gly 35	Ile	Asn	TAT Tyr	Ala	Thr 40	Gly	Asn	Leu	Pro	Gly 45	Cys	Ser	Phe	144
TCT Ser	ATC Ile	TTC Phe	CTT Leu	CTA Leu	GCA Ala	CTT Leu	CTC Leu-	TCG Ser	TGC Cys	TTG Leu	ACT Thr	GTC Val	CCG Pro	GCC Ala	TCG Ser	192

SUBSTITUTE SHEET (RULE 26)

GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp

38693 NB1500

65					70					75					80	
TGC Cys	CCG Pro	AAC Asn	TCT Ser	AGT Ser 85	ATA Ile	GTG Val	TAT Tyr	GAA Glu	GCT Ala 90	gac Asp	CAT His	CAT His	ATC	ATG Met 95	CAT His	. 288
CTA Leu	CCA PTO	GCG	TGT Cys 100	GTG Val	Pro CCT	TGC Cys	GTG Val	AGA Arg 105	ACC The	GGG Gly	AAC Asn	ACC Thr	TCG Ser 110	Arg CGC	TGC Cys	336
TGG Try	GTT Val	CCT Pro 115	TTA Leu	ACA Thr	CCC Pro	ACT Thr	GTG Val 120	GCT Ala	GCC Ala	312 CCC	TAT Tyr	GTT Val 125	GCC	GCG Ala	5zo CC3	384
CTC Leu	GAA Glu 130	TCC Ser	ATG Met	CGG Arg	) CGG	CAC His 135	GTG Val	GAC Asp	TTA Leu	ATG Met	GTG Val 140	GGT Gly	GCC Ala	GCC Ala	ACC Thr	. 432
GTC Val 145	TGC Cys	TCG Ser	GCC Ala	CTG Leu	TAC Tyr 150	ATC Ile	GGA Gly	gac Asp	CTT Leu	TGC Cys 155	GGA Gly	GGT Gly	GTC Val	TTC Phe	CTG Leu 160	- 480
GTC Val	GGG Gly	CAG Gln	ATG Met	TTC Phe 165	ACC Thr	TTC Phe	CGG Arg	CCG Pro	CGC Arg 170	) CGC	CAT His	TGG Trp	ACT Thr	ACC Thr 175	CAG Gl::	<b>528</b>
			TGC Cys 180													576
GCT Ala																579

## (2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

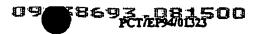
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 10 15 .

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Phe.Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60



Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pr Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
'85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

Val Gly Gln Mer Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

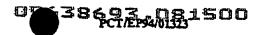
### (2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..579
- (ix) FEATURE:
  - (A) NAME/KEY: mat peptide
  - (B) LOCATION: 1..576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT
Thr Cys Gly Phe Ala Asp Leu Met-Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

CCA GTA GGA GGC GTC GCC AGA GCC TTG GCG CAT GGC GTC AGG GCT GTG 96
Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val



20 25 30

													•••			
GAG	GAC	GGG	ATC	AAT	TAC	GCA	ACA	GGG	AAC	CII	ccc	GGC	TGC	TCC	TTT	144
				Asn												
		35					40					45				
<del></del>	340	<del></del> -		TTG	GT3	بلعثت		***			, <del></del>	~~~	<b>~~</b>	~~~		
				Leu												192
	50					55			~-3	~-	60		•••	~~~	56.	
				CGG												240
	Gla	His	Tyr	yzâ		λla	Sez	Gly	Ile		His	Val	The	Ast	_	
65					70					75					80	
TGC	CCG	AAC	TCC	AGT	ATT	GTG	TAT	GAA	GCC	GAC	CAT	CAC	ATC	ATG	CAC	288
				Ser												
				85					90					95		
																• • • •
				GTG												336
red	FLO	GTÅ	100	Val	PLO	cys	AGT	105	int	GIY	ASI	val	110	Arg	CÀR	
TGG	ATT	CCT	TTA	ACA	CCC	ACT	GTA	GCC	GTC	CCC	TAC	CTC	GGG	GCT	CCY	384
Trp	Ile	Pro	Leu	The	bro	The	Val	λla	Val	SLO	Tyr	Leu	Gly	Ala	Pro	
		115					120					125				
مئت	nce.	TCT	GT3	CGG	CaG	جيم	G=0	63/6	CTG	370	GTG	aca	aca	ccc	300	432
				Arg												432
	130				•	135					140	1				
															TTG	480
	Cys	Ser	Ala	Leu	_	Iie	GIA	Asp	His	Cys 155	Giy	GIÀ	Vai	Phe	Leu 160	
145					150					733					TAA	
GCA	GGG	CAG	ATG	GTC	AGT	TTC	CXX	CCC	CGG	CGT	CAT	TGG	ACT	ACC	CAG	528
Aia	Gly	Gln	Met	Val	Ser	Phe	Gln	220	Arg	Arg	His	ĮIJ	Thr	The	Gln	
				165					170					175		
ርስጥ	***	220	<b>40</b>	***	N TO C	ت د با	باشق	ann	Cac	340	300	<u>ann</u>	Cac	300	ATG	576
															Met	3,0
	-1-		180			-:-		185				1	190			
GCC																579
Ala																

### (2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Thr Cys Gly Phe Ala Asp Leu M t Gly Tyr Ile Pro L u Val Gly Ala

Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser 50 55 60

Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Mec His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys

Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro
115 120 125

Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu 145 155 160

Ala Gly Gln Met Vai Ser Phe Gln Pro Arg Arg Mis Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

- (2) INFORMATION FOR SEQ ID NO: 179:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (ix) PEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..579

PCT/EP94/01323

(xi)	SEQUENCE	DESCRIPTION:	SEO	TD	NO:	179:

ACCTGCGGCT	TCGCCGACCT	CATGGGATAC	ATCCCGCTCG	TAGGCGCCCC	CGTGGGAGGC	60
GTCGCCAGAR	CTCTGGCGCA	TGGCGTCAGG	GCTCTGGAAG	ACGGGATCAA	TTATGCAACA	120
GGGAATCTTC	CTGGTTGCTC	TITCICIATO	TOCOTTOTTG	AACTTCTCTC	GTGCCTGACT	180
GTTCCCGCCT	CAGCCATCCA	CTATCGCAAT	GCTTCGGACG	GITATTATAT	CACCAATGAT	240
TGCCCGAACT	CTAGCATAGT	GTATGAAGCC	GAGAACCACA	TCTTGCACCT	TCCGGGGTGT	300
ATACCCTGTG	TGAAGACCGG	GAATCAGTCG	CGGTGCTGGG	TGGCTCTCAC	CCCCACGCTG	360
GCGGCCCCAC	ACCTACGTGC	TCCGCTTTCG	TCCTTACGGG	CGCATGTGGA	CCTAATGGTG	_ 420
GGGGCCGCCA	CGGCATGCTC	CGCTTTTTAC	ATTGGAGATC	TGTGCGGGG	TGTGTTTTTG	480
GCGGGCCAAC	TGTTCACTAT	CCGGCCACGC	ATTCATGAAA	CCACTCAGGA	CTGCAATTGC	540
TCCATCTACT	CAGGGCACAT	CACGGGTNNN	NUMNINMIN			579

#### (2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLCGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15

Pro Val Gly Val Ala Arg Xaa Leu Ala His Gly Val Arg Ala Leu 20 25 30

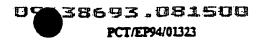
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Ser Leu Leu Glu Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Var Tyr Glu Ala Glu Asn His Ile Leu Ris 85 90 95

Leu Pro Gly Cys Ile Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys 100 105 110



Trp	Val	Ala 115	Leu	Thr	510	Thr	Leu 120	Ala	Ala	Pro	His	Leu 125	Arg	Ala	Pr
Leu	S r 130	Ser	Leu	Arg	Ala	His 135	Val	Asp	Leu	Met	Val 140	Gly	Ala	Ala	Th
A <u>la</u> 145	Cys	Ser	Ala	7he	Tyr 150	Ile	Gly	λsp	Leu	Cys 155	Gly	Gly	Val	Phe	Let
Ala	Gly	Gln	Leu	Phe 165	Thr	Ile	Arg	Pro	<b>Arg</b> 170	Ile	His	Glu	Thr	Thr 175	Gl:
Asp	Cys	Asn	Суs 180	Ser	Ile	Tyr	Ser	Gly 185	Zis	Ile	Thr	Gly	Xaa 190	Xaa	Xaa
Xaa															

- (2) INFORMATION FOR SEQ ID NO: 181:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
      (B) LOCATION: 1..578
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GCGTGCGGCT	TCGCCGATCT	CATGGGATAC	ATCCCGCTCG	TAGGCGCCCC	CGTGGGTGGC	60
GTCGCCAGAG	CCCTGGCGCA	CGGTGTTAGG	GCTGTGGAGG	ACGGGATTAA	CTACGCAACA	120
GGGAATCTTC	CTGGTTGCTC	TTTCTCTATC	TNCCTTCTGG	CACTTCTCTC	GTGCCTGACT	180
GTCCCGGCCT	CGGCTCAGCA	CTACCGGAAT	GTCTCGGGCA	TCTACCACGT	CACCAATGAT	240
TGCCCGAATT	CCAGCATAGT	GTATGAAGCC	GATCACCACA	TCATGCACTT	ACCAGGGTGC	300
ATACCCTGCG	TGAGGACCGG	GAACGTTTCG	CGCTGCTGGG	TATCTCTGAC	ACCTACTGTG	360
GCTGCTCCCT	ACCTCGGGGC	TCCGCTTACG	TCGCTACGGC	GGCATGTGGA	TTTGATGGTG	420
GGTGCAGCCA	CCCTTTGCTC	TGCCCTCTAC	GTCGGAGACC	TCTGTGGAGG	TGTCTTCCTA	480



GTGGGACAGA TGTTCACCTT CCAGCCGCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540
TCCATTTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

### (2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (8) TYPS: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:
- Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15
- Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30
- Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45
- Ser Ile Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60
- Ala Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80
- Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95
- Leu Pro Gly Cys Ile Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys
- Trp Val Ser Leu Thr Pro Thr Val Ala Ala Pro Tyr Leu Gly Ala Pro 115 120 125
- Leu Thr Ser Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140
- Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160
- Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175
- Asp Cys Asn Cys Ser Ile Tyr Val Gly Ris Ile Thr Gly His Arg Met 180 185 190

Ala

# (2) INFORMATION FOR SEQ ID NO: 183:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \$79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

### (ix) FEATURE:

- (A) NAME/KEY: COS
- (B) LOCATION: 1..579

### (ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

ACC Thr	cys	GGC Gly	TTT	GCC Ala 5	GAC <b>As</b> p	CTC Leu	ATG Met	GGA Gly	TAC Tyr 10	ATC Ile	CCG Pro	CTC Leu	GTA Val	GGC Gly 15	GCC Ala	48
CCT	GTG Val	GGT Gly	GGC Gly 20	GTC Val	GCC Ala	AGG Arg	GCC Ala	CTA Leu 25	GAA Glu	CAC His	GGT Gly	GTT Val	AGG Arg 30	GCT Ala	GTG Val	96
GAG Glu	GAC Asp	GGT Gly 35	ATT Ile	AAT Asn	TAT Tyr	GCA Ala	ACA Thr 40	GGG Gly	AAT Asn	CTC Leu	CCC	GGT Gly 45	TGC Cys	TCT Ser	TTT Phe	144
TCT Ser	ATC Ile 50	TCC Ser	CTC Leu	TTG Leu	GCA .Ala	CTT Leu 55	CTT Leu	TCG Ser	TGC Cys	CTG Leu	ACT Thr 60	GTT Val	Pro	ACC Thr	TCA Ser	192
GCC Ala 65	GTC Val	AAC Asn	TAT Tyr	CGC Arg	AAC Asn 70	GCC Ala	TCG Ser	GGC Gly	GTC Val	TAT Tyr 75	CAT His	ATC Ile	ACC Thr	AAT Asn	GAC Asp 80	240
TGC Cys	CCG Pro	AAT Asn	TCG Ser	AGC Ser 85	ATA Ile	GTG Val	TAC Tyr	GAG Glu	GCT Ala 90	GAC Asp	TAC Tyr	CAC His	ATC Ile	CTA Leu 95	CAC His	288
CTC Leu	CCT Pro	GGG Gly	TGC Cys 100	TTA Leu	CCC	TGC Cys	GTG Val	AGG Arg 105	GTT Val	GGG G1y	TAA Tea	CAG Gln	TCA Ser 110	<b>C</b> GC <b>A</b> TG	TGC Cys	336
TGG Tro	GTG Val	GCC	CTT	ACT	CCC	ACC	GTG	GCG	GCG Ala	CCT	TAC	GTT	GGT	GCT	CCG	384

		115					120					125				
					AGT Ser											432
	130		-			135	•••	,			140	,		~	•	
GTG	TGC	TCC	GCT	CTT	TAC	ATC	GGG	GAC	CIG	TGC	GGT	GGC	GTA	TTT	TTG	480
Va:	CAR	Sez	λla	Leu	Tyr	Ile	GLY	<b>Za</b> Ş	Leu	C\a	Gly	Gly	Val	2he	Leu	
145					150					155					160	
GTT	GGT	CAG	ATG	m	TCT	TTC	CAG	CCG	CGA	CGC	CAC	TGG	ACC	ACG	CAG	528
Val	Gly	Gln	Met	Phe	Ser	Phe	Gla	Pro	Arg	Arg	His	Trp	Thr	Thr	Gla	
				165					170					175		
					ATC											576
Asp	Cys	Asn	-	Ser	Ile	Tyr	λla	•	His	Val	Thr	Gly		Arg	Met	
			180					185					190			
GCA											•					- 579
A 1 =																

- (2) INFORMATION FOR SEQ ID NC: 184:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met

Ala

- (2) INFORMATION FOR SEQ ID NO: 182:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 192 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:
- Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15
- Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30
- Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45
- Ser Ile Ser Phe Trp His Phe Ser Arg Ala . Leu Ser Arg Pro Arg 50 55 60
- Leu Ser Thr Thr Gly Met Ser Arg Ala Ser Thr Thr Ser Pro Met Ile
  65 70 75 80
- Ala Arg Ile Pro Ala . Cys Met Lys Pro Ile Thr Thr Ser Cys Thr 85 90 95
- Tyr Gln Gly Ala Tyr Pro Ala Gly Pro Gly Thr Phe Arg Ala Ala 100 105 110
- Gly Tyr Leu His Leu Leu Trp Leu Leu Pro Thr Ser Gly Leu Arg
- Leu Arg Arg Tyr Gly Gly Met Trp Ile * Trp Trp Val Gln Pro Pro 130 135 140
- Phe Ala Leu Pro Ser Thr Ser Glu Thr Ser Val Glu Val Ser Ser 145 150 155 160
- Trp Asp Arg Cys Ser Pro Ser Ser Arg Ala Ala Thr Gly Pro Leu Arg
- Thr Ala Thr Ala Pro Phe Thr Ser Ala Thr Ser Gln Ala Thr Glu Trp

180

190

121	INFORMATION	FCR	820	TD	NO .	185
141	INFURMALIUM	FUR	350	-11	av:	762

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEG ID NO: 185:

ACT TGC GGC	TTT GCC GAC	TTC ATG GGA TAC ATC	CCG CTC GTA GGC GCC 48
Thr Cys Gly	Phe Ala Asp	au Met Gly Tyr Ile	Pro Leu Val Gly Ala
1	5	10	15

CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val

20 25 30

GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC 144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser

GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp

70

75

80

TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His

95

CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys

100 105 110

TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA 384

Trp	Val	Ala 115	Leu	Ser	Pro	Thr	Val 120	Ala	Ala	Pro	Tyr	Ile 125		Ala	Pro	
GTT Val	GAA Glu 130	TCC	TTC Phe	CGG Arg	AGA Arg	CAC His 135	GTG Val	gac Asp	ATG Met	ATG Met	GTG Val 140	GGC Gly	GCT Ala	GCT Ala	ACT Thr	432
GTG Val 145	TGC Cys	TCC Ser	GCT Ala	CTC Leu	TAT Tyr 150	ATT Ile	GGG Gly	GAC Asp	TTG Leu	TGT Cys 155	GGT Gly	GGC Gly	GTA Val	TTC Phe	TTG Leu 160	480
GTT Val	ggt Gly	CAG Gln	ATG Mec	TTT Phe 165	TCT Ser	TTC Phe	CGG Arg	CCA Pro	CGA Arg 170	CGC Arg	CAC	TGG Trp	ACT Thr	ACG Thr 175	CAG Gln	<b>528</b>
GAC Asp	TGC Cys	AAT Asn	TGT Cys 180	TCC Ser	ATC Ile	TAC Tyr	GCG Ala	GGG Gly 185	CAC His	ATC Ile	ACT Thr	GGC Gly	CAC His	GGA Gly	ATG Met	57 <b>6</b> -
GCA Ala																579

- (2) INFORMATION FOR SEQ ID NO: 186:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp 65 70 75 80

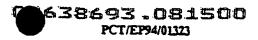
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asa Glm Ser Arg Cys

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

e.	
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr 130 140	
Val Cys S r Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160	
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln 165 170 175	
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met 180 185 190	
Ala	
(2) INFORMATION FOR SEQ ID NO: 187:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 579 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1579	
(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1576	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:	
ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC  Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  1 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG  Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  20  25  30	
GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT-TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTT-TCG TGC CTG ACT GTT CCC ACC TCG  Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	

GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC



Ala 69	Val	. Asn	Tyr	Arg	<b>Asn</b> 70	Ala	Ser	Gly	11	Tyr 75		Ile	Thr	Asn	Asp 80		
Cys	PIG	ASI	ser	AGC Ser 85	TTE	Val	Tyr	Glu 	Thr 90	Glu	His	His	Il	Leu 95	His		288
CTC	Pro Pro	GGG Gly	TGT Cys	TTA Leu	520 CCC	CÀa 12C	GTS Val	AGG Arg 105	GII Val	GGG Gly	AAT Asn	CAG Gla	TCA Ser 110	CGC CGC	TGC Cys		336
TGG	GTG Val	GCC Ala 115	CTC Leu	ACT Thr	bio CCC	ACC Thr	GTG Val 120	GC3 Ala	GCG Ala	CCT Pro	TAC Tyr	ATC Ile 125	GGC Gly	GCT Ala	CCG Pro		384
CTT Leu	GAA Glu 130	TCC Ser	CTC Leu	CGG Arg	AGT Ser	CAT His 135	GTG Val	GAT Asp	CTG Leu	ATG Met	GTA Val 140	GGT Gly	GCC Ala	GCT Ala	ACT Thr	-	432
GCG Ala 145	TGC Cys	TCC Ser	GCT Ala	CTT Leu	TAC Tyr 150	ATC Ile	GGA Gly	GAC Asp	CTG Leu	TGC Cys 155	GGT Gly	GGC Gly	GTA Val	TTT Phe	TTG Leu 160		480
GTT Val	GGT Gly	CAG Gln	Met	TTC Phe 165	TCT Ser	TTC Phe	CAG G1::	Pro CCG	CGG Arg 170	CGC	CAC His	TGG Trp	ACT Thr	ACG Thr 175	CAG Gln		529
GAC Asp	TGC Cys	Asn	TGT Cys 180	TCC Ser	ATC Ile	TAC Tyr	Ala	GGG Gly 185	CAC His	GIT Val	ACG Thr	GGC Gly	CAC His 190	AGG Arg	ATG Met		576
GCA Ala																	579

# (2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

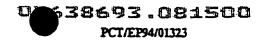
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60



Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Il Val Tyr Glu Thr Glu His His Ile Leu His 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..579
- (ix) FEATURE:
  - (A) NAME/KEY: mat_peptide
  - (B) LOCATION: 1..576
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

48



CCC	GT	GGG	GGC	GTC	GCC	AGG	GCC	CTG	CCS	CAT	GGC	GTC	164	CCT	CTC		
Pro	Val	Gly	Gly	Val	Ala	Ara	Ala	I=0U	Ala	H: e	Gly	Val	7	91.	010	3	96
		•	20			3		25		444	GLY	AgT		ALA	Val		
													30				
GAG	GAC	GGG	ATT	220	T3 =	aca	803	~~~									
Gli	Aco	C1.	ATT	~~~		31-	MLA.	-	- AAT	CIT	CCC	GGT	TGC	TCI	TTC	14	4
GIU	MSD	GIÀ	Ile	AS:	IAT	ALA	The	GTA	ASD	Leu	Pio	Gly	Cys	Ser	Phe		
		35					40					45					
TCI	ATC	TTC	CTC	CIG	CCX	CII	CII	TÇG	ICC	CTC	ACT	GTC	CCA	GCG	TCA	19	2
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	CA2	Leu	The	Val	Pro	Ala	Ser		•
	50					55					60						
GCT	GAG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	ATC	TAT	CZC	370	300	837	CAC	24	
Ala	Glu	His	Tyr	Ara	Asa	Ala	Ser	Glv	71.	Topo	2:2	710	7L-	~~·	CAC	24	U
65					70			,		75	5	116	IRI	ASI			
					. •					/3					80		
TCT	cca	አጻጥ	TCC	200			~~~										
~~	200		TCC	AUG.	GIA	Gic	TAT	CAN	ACT	GAC	CYC	CAT	ATA	TTG	CAC	28	8
Cys	PIO	ASI	Ser	ser	val	Vai	TYI	Glu	The	γsɔ̈	His	His	Ile	Leu	His	•-	
				85					90					95			
TIG	CCG	GGG	TGC	GTA	CCC	TGC	GTG	AGG	GCC	GGG	AAC	GTG	TCT	CGT	TGC	33	6
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Ala	Glv	ÀS::	Val	Ser	Ara	CVS		_
			100					105		•			110		•.•		
TGG	ACG	CCG	GTA	ACA	CCT	ACG	GTG	c~	acr	رسي	TCC		~~~		000		
T	The	Pro	Va1	The	D~0	The	Ua?	313	33.	11-1	****	A46	GAL	GC.	-	. 38	4
		115		••••				~~a	~_a	Vd_	261		ASÇ	ATA	Pro		
		113					120					125					
	~~~																
Cit	GAG	TCC	TTC	CGG	CGG	CAT	GTG	GAC	CTA	atg	GTA	ggt	GCG	GCC	ACC	43	2
Leu	Glu	Ser	Phe	yrg	ATT	Ris	Vai	ζεκ	Leu	Met	Val	Gly	Ala	Ala	Thr		
	130					135					140						
GTG	TGT	TCT	GTC	CTC	TAT	GTT	GGA	GAC	CTC	TGT	GGA	GGT	GCT	TTC	CTA	48	'n
Val	Cys	Ser	Val	Leu	Tyr	Val	Glv	σzk	Leu	Cvs	Glv	Glv	Ale	Dhe	7.011	40	•
145	_				150		•	•		155	;	,			160		
															100		
GTG	GGG	CAG	ATG	TTC	ACC	TTC	CaG	ccc	~~		C) C	200					_
Val	Gly	Gla	Mae	Bho	Th-	Dha	C1-	200				166	ACC	ACG	CAG	52	8
	UL,	GIII	Met		****	FIIG	GTU	123		YZŽ	272	1.	Thr		Gln		
				165					170					175			
~ >**	-																
CAT	IGT	AAT	TGC	TCC	ATC	TAT	ACT	GGC	CYL	ATC	ACC	GGÇ	CAC	AGG	ATG	57	6
Asp	Cys		Cys	Ser	Ile	Tyr	Thr	Gly	His	Ile	The	Gly	His	Arg	Met		
			180					185					190	-			
GCG													•			57	9
Ala																•	-

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala Eis Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro

Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

- (2) INFORMATION FOR SEQ ID NO: 191:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS



(B) LOCATION: 1..289

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..286

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ATG Met 1	AGC Ser	ACG	AAT Asn	CCT Pro 5	aaa Lys	CCT Pro	CAA Gln	AGA Arg	AAA Lys 10	ACE Thr	AAA Lys	CGT	AAC Asti	ACC Thr 15	AAC Asn		48
CGC Arg	CGC Arg	Pro CCC	ATG Met 20	gac Asp	GTT Val	AAG Lys	TTC Phe	CCG Pro 25	G] Y	GGT Gly	GGC Gly	CAG Gln	ATC Ile 30	GTT Val	GGT Gly		96
GGA Gly	GTT Val	TAC Tyr 35	TTG Leu	TTG Leu	9TO	Yza CCC	AGG Arg 40	GGC	CCC	λGG	TTG Leu	GGT Gly 45	GTG Val	yrg ccc	GCG Ala		- 144
ACT Thr	AGG Arg 50	AAG Lys	ACT Thr	TCG Ser	GAG Glu	CGG Arg 55	TCG Ser	CAA Gln	Pro	CGT Arg	GGG Gly 60	AGA Arg	CGT Arg	CAG Gln	510 CCI		192
ATC Ile 65	CCC Pro	AAG Lys	GCA Ala	CGT Arg	CGA Arg 70	TCT Ser	GAG Glu	GGA Gly	AGG Arg	TCC Ser 75	TGG Trp	GCT Ala	CAG Gln	CCC	GGG Gly 80		240
TAC Tyr	CCA Pro	TGG Trp	CCT Pro	CTT Leu 85	TAC Tyr	GGT Gly	TAA Asn	GAG Glu	GGT Gly 90	TGT Cys	GGG Gly	TGG Trp	GCA Ala	GGA Gly 95	Irp	G	289

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly

243



65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp 85 90 95

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

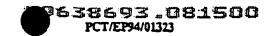
(A) NAME/KEY: CDS
(B) LOCATION: 1..498

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

					AAA											48
	Ser	Thr	Asn		Lys	Pro	Gln	Arg	-	The	Lys	Arg	Asn		Asn	
1				5					10					15		
					GTA											96
Arg	Arg	Pro		V ED	Val	Lys	Pne		GIY	GIĀ	GIY	GII		vai	GIÅ	
			20					25					30			
GGA	GTT	TAC	TTG	TTG	CCG	CGC	AGG	ccc	ccc	cca	TTG	GGT	GTG	CGC	GCG	144
					Pro								-			
,		35			•••	3	40	,		3		45		3		
												•••				
ACT	CGG	AAG	ACT	TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGC	AGG	CGT	CAA	CCT	192
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	EIA	Gly	Arg	Arg	Gln	Pro	
	50	•				55				_	60	_	_		•	
															•	
ATC	CCC	AAG	GCG	CGC	CGG	TCC	GAG	GGC	AGG	TCC	TGG	GCG	CAA	GCC	GGG	240
Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Ala	Gly	
65					70					75					80	
TAC	CCC	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGT	GGG	TGG	GCA	GGG	TGG	288
TYT	Pro	Irp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	
				85					90					95		
																226
CTC	CTG	TCT	CCI	CGC	GGC	TCT	CGG	CCA	TCT	TGG	GGC	CCA	AAT	GAT	CCC	336



Leu	Leu	Ser	Pro 100	Arg	Gly	Ser	Arg	Pro 105	Ser	فتر	Gly	Pro	Asn 110	Asp	Pro	
CGG	CGG Arg	AGA Arg 115	TCG Ser	CGC Arg	aat Asn	CTG Leu	GGT Gly 120	AAG Lys	GTC Val	ATC Ile	GAT Asp	ACC Thr 125	CTG Leu	ACG Thr	TGC Cys	384
GGC Gly	TTC Phe 130	GCC Ala	GAC Asp	CTC Leu	ATG Met	GGA Gly 135	TAC Tyr	ATC Ile	CC3	CTC Leu	GTG Val 140	GGC Gly	GCC Ala	CCC Pro	GTC Val	432
GGG Gly 145	et ^y eec	GTC Val	GCC Ala	AGG Arg	GCC Ala 150	CTG Leu	GCG Ala	CAT His	GGC Gly	GTC Val 155	AGG Arg	GCT Ala	GTG Val	GAG Glu	GAC Asp 160	480
GGG . Gly																498

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro So 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro 100 105 110

Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val



288

336

								2	245							
Gl ₃	Gly	Val	Ala	Arg	Ala 150	Leu	Ala	His	Gly	Val 155	Arg	Ala	Val	Glu	Asp 160	
Gly	'Ile	Asn	Tyr	Arg 165	Gln											
(2)	INF	orma	TION	FOR	SZQ	ID 1	NO:	195:								
	į)	€. €:	A) L B) T C) S'	CE C ENGT: YPE: TRANI OPOLO	H: S' DUC DEDN	79 bi leic ESS:	ase pacions acid	pair: d								
	(ii) MO	LECU:	LE T	PE:	CDN	A.									
	(111) HY	POTH	ETIC	AL: I	NO										•
	(iii) an	TI-S	ENSE	: NO											
	(ix	(2		E: AME/I			579									
	(ix	C		e: Ame/i Ocati				tide								
	(xi)) SE	QUENC	CE DS	esca:	EPTIC	ON: !	SEQ :	ID NO): 1 <u>9</u>	95 :		•			
ACG Thr 1	TGC Cys	GGA Gly	TTC Phe	GCC Ala 5	GAC Asp	CTC Leu	GTG Val	GGG Gly	TAC Tyr 10	ATC Ile	CCG Pro	CTC Leu	GTA Val	GGC Gly 15	GGC Gly	48
CCC Pro	GTT Val	GGG	GGC Gly 20	GTC Val	GCA Ala	AGG Arg	GCT Ala	CTC Leu 25	GCA Ala	CAT His	GGT Gly	GTG Val	AGG Arg 30	GTT Val	CTT Leu	96
GAG Glu	GAC	GGG Glv	GTG Val	TAA	TAT	GCA	ACA Thr	GGG G1 v	AAT	CTG	CCT	GGT	TGC	TCT Ser	TTC	144
		35	***		-7-		40	7	nau	Jeu	-10	45	cys	341	rne	
														GCC Ala		192
GCA Ala 65	GTT Val	CCC	TAC Tyr	CGA Arg	AAT Asn 70	GCC Ala	TCT Ser	GGG Gly	ATC Ile	TAT Tyr 75	CAT His	GTC Val	ACC Thr	AAT Asn	GAT Asp 80	240

SUBSTITUTE SHEET (RULE 26)

TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His

GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC

90

85



Ala	Pro	Gly	Cys 100	Val	Pro	Cys	Val	Arg	Lys	Asp	Asn	Val	Ser 110	Arg	Суз		
TGG Trp	GTC Val	CAA Gln 115	ATT Ile	ACC Thr	510 CCC	ACG Thr	CTG Leu 120	TCA Ser	GCC	Pro	AGC Ser	TTC Phe 125	GGA Gly	GCA Ala	GTC Val		384
ACG Thr	GCT Ala 130	Pro	CTT Leu	CGG Arg	AGA Arg	GCC Ala 135	GTT Val	gat Asp	TAC Tyr	TTG Leu	GTG Val 140	GGA Gly	GGG Gly	GCT Ala	GCC Ala		432
CTC Leu 145	TGC Cys	TCC Ser	GCG Ala	TTA Leu	TAC Tyr 150	GT: Val	GGA Gly	GAC Asp	GCG Ala	TGT Cys 155	GGG Gly	GCA Ala	CTA Leu	TTT Phe	TTG Leu 160		480
Val	Gly	Gln	Mec	Phe 165	ACC Thr	TÀI	Arg	Pro	Arg 170	Gln	His	Ala	Thr	Val	Gln		528
GAC Asp	Cys	AAC Asn	TGT Cys 180	TCC Ser	ATC Ile	TAC Tyr	AGT Ser	GGC Gly 185	CAC His	GTC Val	ACC Thr	GGC Gly	CAT His 190	CAG Gln	ATG Met	!	576
GCA Ala																!	579

- (2) INFORMATION FOR SEQ ID NO: 196:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

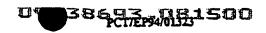
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His 85 90 95

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys 100 105 110



Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 197:

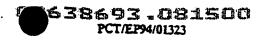
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ACT	TGC	GGC	TIT	GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CIC	GTA	GGC	GCC	48
Thr	Суз	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	
1	•	-		5					10					15		

CCC GTG GGT GGC GTC GCC	AGA GCC CTG GAA CAT GGT	GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala	Arg Ala Leu Glu His Gly	Val Arg Ala Val	
20	25	30	

GAG GAC GGC ATC AAT TAT Glu Asp Gly Ile Asn Tyr 35	GCA ACA GGG AAT CT Ala Thr Gly Asn Le 40	C CCC GGT TGC TCT u Pro Gly Cys Ser 45	TTC 144 Phe
--	--	--	----------------

TOT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG 192



Se	7 Ile 50	ty:	Leu	Leu	Ala	Leu SS	Leu	Sez	Cys	Leu	Thi 60		Pro	Thr	Ser		
65				wid	70	ALA	Ser	. er l	Val	75	Ris	Val	Thr	Asn	GAC Asp	:	240
-,-			361	85	176	AGI	ıyı	Glu	90	Asp	His	His	Ile	Leu 95		:	288
		or,	100	neu	PIQ	Cys	val	105	Val	Gly	Asn	Gln	Ser 110	Arg		;	336
TGG	GTG Val	GCC Ala 115	CTC Leu	TCT Ser) Pro	ACC Thr	GTG Val 120	GCG Ala	GCG Ala	CCT Pro	Tyr	ATC Ile 125	GGT Gly	GCT Ala	CCA Pro		884
GTT Val	GAA Glu 130	TCC Ser	TTC Phe	yra CCC	AGA Arg	CAC His 135	GTG Val	GAC Asp	ATG Met	ATG Met	GTG Val 140	GGC Gly	GCT Ala	GCT Ala	ACT Thr	4	32
145	-,-	962	714	pen	TAT Tyr 150	TTG	GIÀ	Ysb	Leu	Cys 155	Gly	Gly	Val	Phe	Leu 160	. 4	80
	GL y	9 111	nec	165	TCT :	₽ne	Arg	Pro	Arg 170	Arg	His	Trp	Thr	Thr 175	Gln	5	28,
GAC Asp	TGC . Cys .	MSII	TGT Cys 180	TCC : Ser :	ATC ' Ile '	TAC Tyr .	Ala	GGG Gly : 185	CAC His	ATC Ile	ACT Thr	Gly	CAC His 190	GGA Gly	ATG Mec	5	76
GCA Ala																S	79

- (2) INFORMATION FOR SEQ ID NO: 198:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 10 15

Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

45

35

40

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

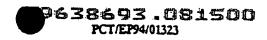
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1470
- (ix) FEATURE:
 - (A) NAME/KEY: mat peptide
 - (B) LOCATION: 2..1467
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:



A	TCA Ser 1	CCA Pro	CCG Pro	GAG Glu	CTT Leu 5	CTA Leu	TCA Ser	CAT :	ACT (CCX (Pro : 10	CTT Leu	ACG (GCA : Ala :	AGT :	TCC Ser 15	46
TT Le	G CI	G AI	G GA E Gl	G GG u Gl; 2	y va	r ca l Gl	G GC	G GCC	G CGG Arg	J Me:	G AC	G TG	A TC: Se:	A TAT	GCG Ala	94
	- 00	• ~.	3:	5	s May	j in	. 520	40) }	> Phe	Le	u Gly	45	Ala S	CTG Leu	
		5	0	, 41.	· ALS	AES	5 Let	i GTA	Leu	Gl;	'Se:	Sez 60	: Se:	T	CCA Pro	190
•••	6	5	J LE	ı Pic	AL a	70		Gln	Arg	520	75 75	Pro	Thr	Ser	AGG Arg	238
AAC Lys 80	•••	Pro	TGC Cys	CTC	AGG Arg 85	Wid	GGG Gly	AGG Arg	TTC	90 CCI	Sez	ACG Thr	GCA Ala	GAG Glu	CCA Pro 95	286
Phe	Pro	TTO Leu	: CTI	TTA Leu 100	•	AGG Arg	GTG Val	GTA Val	GGC Gly 105	Ile	TCA Ser	TCT Ser	TCT Ser	GCC Ala 110	ATT Ile	. 334
CCA Pro	AGA Arg	Lys	AAT Asn 115	. vai	ATG Mes	AAC Asn	TCG Ser	CCA Pro 120	AGC Ser	AAC Asn	TGA	CCA Pro	GCC Ala 125	TGG Trp	GCG Ala	382
TGA	ACG	CCG Pro 130	120	CAT His	ATT Ile	ATA Ile	GAG Glu 135	GTC Val	TAG	ACG Th .	TCG Ser	CCG Pro 140	TCA Ser	TAC Tyr	CCA Pro	430
CAA Gln	CAG Gln 145	GAG Glu	ACG Thr	TGG Trp	TCG Ser	TGT Cys 150	GCA Ala	GCA Ala	CCG Pro	ACG Thr	CGC Arg 155	TCA Ser	TGA •	CGG Arg	GAT Asp	478
TCA Ser 160	CCG Pro	GCG Ala	ACT	TTG Leu	ATT Ile 165	CTG Leu	TCA Ser	TAG	ACT The	GCA Ala 170	ACT Thr	CCG Pro	CCG Pro	TCA Ser	CTC Leu 175	526
AGA Arg	CGG Arg	TGG Trp	ACT Thr	TCA Ser 180	GTC Val	TTP TGG	ATC Ile	CCA Pro	CTT Leu 185	TTA Leu	CCA Pro	TTG Leu	AGA Arg	CTA Leu 190	CCA Pro	574
CAG Gln	TGC Cys	Pro	AGG Arg 195	ACG Thr	CAG Gln	TGT Cys	CCA Pro	GAA Glu 200	GCC Ala	AGC Ser	GTT Val	GGG Gly	GCC Ala 205	GCA Ala	CGG	. 622
GGA Gly	GAG Glu	GTA Val 210	GGC GGC	ACG Thr	GCA Ala	TAT Tyr	ACC Thr 215	GGT Gly	ATG Met	TCT Ser	CGG	CTG Leu 220	GAG Glu	AGA Arg	GAC Asp	670
CGT Arg	CTG Leu	GCA Ala	TGT Cys	TCG Ser	ACT Thr	CCG Pro	TGG Trp	TGC Cys	TCT Ser	GTG Val	AGT Se:	GCT Ala	ACG Thr	ATG Me:	CCG Pro	718



	225					230					235					
GAT Asp 240	GTG Val	CAT His	GGT Gly	ACG Thr	ATC Ile 245	TGA	CTC	CTG Leu	Pro	AGA Arg 250	CTA Leu	CCG Pro	TGA •	GGT Gly	TGC Cys 255	766
gcg Ala	CTT Leu	ACT Thr	aaa Lys	CAC His 260	Pro CCC	YZZ CGG	GCT ALB	000 710	TGT Cys 265	CTG Leu	TCA Ser	GGA Gly	CCA Pro	TTT Phe 270	GGA Gly	814
					GTT Val											862
					ACA Thr											910
					CTG Leu											958
					ATG Met 325											1005
					TAC Tyr											1054
					ACC Thr											1102
					AGC Ser											1150
					TGC Cys											1198
					GGG Gly 405											1246
					gat A sp											1294
					CGT Arg											1342
					ACG Thr											1390

Ala	Ala 465	ACG Thr	TCT Ser	Val	Trp	AAC ASB 470	AAG Lys	GCT Ala	GAG Glu	CAG Gla	TTC Phe 475	TGG Trp	CCA Pro	CAT His	ACA Thr	1438
TGT Cys 480	GGÀ Gly	ACT Thr	TCA Ser	TCA Ser	GTG Val 485	gga Gly	TAC Tyr	TAK RSA	AAT Asn	AG						1470

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

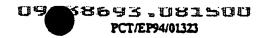
(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TGTGCCAGGA	CCATCACCAC	CGGAGCTTCT	ATCACATACT	CCACTTACGG	CAAGTTCCTT	60
GCTGATGGAG	GGTGTTCAGG	CGGCGCGCAT	GACGTGATCA	TATGCGACGA	GTGCCATTCC	120
CAGGACGCCA	CEACCATTCT	TGGGATAGGC	ACTGTCCTTG	ACCAGGCAGA	GACGGCTGGA	180
GCTAGGCTCG	TCGTCTTGGC	CACGGCCACC	CCTCCCGGCA	GTGTGACAAC	GCCCACCCC	240
AACATCGAGG	AAGTGGCCCT	GCCTCAGGAG	GGGGAGGTTC	CCTTCTACGG	CAGAGCCATT	300
CCCCTTGCTT	TTATAAAGGG	TGGTAGGCAT	CTCATCTTCT	GCCATTCCAA	GAAAAAATGT	360
GATGAACTCG	CCAAGCAACT	GACCAGCCTG	GGCGTGAACG	CCGTGGCATA	TTATAGAGGT	420
CTAGACGTCG	CCGTCATACC	CACAACAGGA	GACGTGGTCG	TGTGCAGCAC	CGACGCGCTC	480
ATGACGGGAT	TCACCGGCGA	CTTTGATTCT	GTCATAGACT	GCAACTCCGC	CGTCACTCAG	540
ACGGTGGACT	TCAGTCTGGA	TCCCACTTTT	ACCATTGAGA	CTACCACAGT	GCCCCAGGAC	600
GCAGTGTCCA	GAAGCCAGCG	TTGGGGCCGC	ACGGGGAGAG	GTAGGCACGG	CATATACCGG	660
TATGTCTCGG	CTGGAGAGAG	ACCGTCTGGC	ATGTTCGACT	CCGTGGTGCT	CTGTGAGTGC	720
TACGATGCCG	GATGTGCATG	GTACGATCTG	ACTCCTGCCG	AGACTACCGT	GAGGTTGCGC	780
GCTTACNTAA	ACACCCCGG	GCTCCCTGTC	TGTCAGGACC	ATTTGGAATT	CTGGGAGGGG	. 840
GTGTTCACGG	GGCTCACTAA	CATCGACGCT	CACATGCTGT	CACAGACCAA	ACAGGGTGGG	900
GAGAATTTCC	CATACCTTGT	AGCGTACCAA	GCAACAGTCT	GTGTTCGCGC	GAAAGCGCCC	960



CCCCCCAGCT	GGGACACAAT	GTGGAAATGC	ATGCTCCGTC	TCAAACCGAC	NTTAACTGGC	1020
CCTACTCCCC	TCTTGTACAG	GCTGGGGCCC	GTCCAGAATG	AGATCACACT	GACGCACCCC	1080
ATCACCAAGT	ACATTATGGC	TTGCATGTCT	GCGGACTTGG	AGGTCATTAC	CAGCACTTGG	1140
GTTCTGGTGG	GGGGCGTTGT	GGCGGCCCTG	GCGGCCTACT	GCTTGACGGT	GGGTTCGGTA	1200
GCCATAGTCG	GTAGGATCAT	CCTCTCTGGG	AAACCTGCCA	TCATTCCCGA	TAGGGAGGTA	1260
TTATACCAGC	AATTTGATGA	GATGGAGGAG	TECTCEGCCT	CGTTGCCCTA	TATGGACGAA	1320
ACACGTGCCA	TTGCCGGACA	ATTCAAAGAG	AAAGTGCTCG	GCTTCATCAG	CACGACCGGC	1380
CAGAAGGCTG	AAACTCTGAA	GCCGGCAGCC	ACGTCTGTGT	GGAACAAGGC	TGAGCAGTTC	1440
TGGNCCACAT	ACATGTGGAA	CTTCATCAGT	GGGATACAAT	AATAG		1485

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr

1 10 15

Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val 20 25 30

Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly 35 40 45

Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val 50 55 60

Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro 65 70 75 80

Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr 85 90 95

Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile 100 105 110

Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr 115 120 125

Ser Leu Gly Val Asm Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala 130 135 140

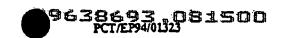
Val 145	Ile	Pro	Thr	Thr	Gly 150	Asp	Vàl	. Val	. Val	Cys 155	Sec	The	Asp	Ala	Leu 160
Mec	The	Gly	Phe	Thr 165	Gly	Asp	Phe	Asp	Ser 170	Val	Ile	Asp	Cys	Asn 175	
Ala	Val	Thr	Gla 180	Thr	Val	λsp	Phe	Ser 185	Leu	de ∜∶	Pro	Thr	Phe 190	Thr	Ile
		133		Val			200					205			
Gly	Arg 210	Thr	Gly	Arg	Gly	Arg 215	His	Gly	Ile	ıàı	Arg 220	Tyr	Val	Ser	Ala
Gly 225	Glu	Arg	Pro	Ser	Gly 230	Met	Phe	Asp	Ser	Val 235	Val	Leu	Cys	Glu	Cys 240
Tyr	Asp	Ala	Gly	Cys 245	Ala	ĮTĮ	Tyr	Asp	Leu 250	Thr	Pro	Ala	Glu	Thr 255	Thr
Val	Arg	Leu	Arg 260	Ala	Tyr	Xaa	Asn	Th: 265	Pro	Gly	Leu	Pro	Val 270	Cys	Gln
Asp	His	Leu 275	Glu	Phe	Trp	Glu	Gly 280	Val	Phe	Thr	Gly	Leu 285	Thr	As:	Ile
Ąsp	Ala 290	His	Met	Leu	Ser	Gla 295	Thr	Lys	Gln	Gly	Gly 300	Glu	Asa	Phe	Pro
Tyr 305	Leu	Val	Ala	Tyr	Gla 310	Ala	Thr	Val	Cys	Val 315	Arg	Ala	Lys	Ala	Pro 320
Pro	PTO	Ser	ĮÞ	Asp 325	Thr	Met	Ţŗp	Lys	Cys 330	Mec	Leu	Arg	Leu	Lys 335	920
Xaa	Leu	Thr	Gly 340	Pro	Thr	PTO	Leu	Leu 345	Tyr	Arg	Leu	Gly	Pro 350	Val	Gln
Asn	Glu	Ile 355	Thr	Leu	Thr	His	Pro 360	Ile	Thr	Lys	Tyr	Ile 365	Met	Ala	Cys
Met	Ser 370	Ala	qaA	Leu	Glu	Val 375	Ile	Thr	Ser	Thr	380 dzl	Val	Leu	Val	Gly
Gly 385	Val	Val	Ala	Ala :	Leu . 390	Ala	Ala	Tyr	Cys	Leu 395	Thr	Val	Gly _.	Ser	Val 400
Ala	Ile	Val	Gly	Arg : 405	Ile	Ile	Leu	Ser	Gly 410	Lys	Pro	Ala	Ile	Ile 415	Pro

SUBSTITUTE SHEET (RULE 26)

. :

Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser 420 425 430

Ala Ser Leu Pro Tyr Met Asp'Glu Thr Arg Ala Ile Ala Gly Gln Phe 435 440 445



Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe 465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1485 base pairs
 - (B) TYPE: mucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TGTGCCAGGA	CCATCACCAC	CGGAGCTTCT	ATCACATACT	CCACTTACGG	CAAGTTCCTT	60
GCTGATGGAG	GGTGTTCAGG	CGGCGCGTAT	GACGTGATCA	TATGCGACGA	GTGCCATTCC	120
CAGGACGCCA	CCACCATTCT	TGGGATAGGC	ACTGTCCTTG	ACCAGGCAGA	GACGGCTGGA	180
GCTAGGCTCG	TCGTCTTGGC	CACGGCCACC	CCTCCCGGCA	GTGTGACAAC	GCCCCACCCC	240
AACATCGAGG	AAGTGGCCCT	GCCTCAGGAG	GGGGAGGTTC	CCTTCTACGG	CAGAGCCATT	300
CCCCTTGCTT	TTATAAAGGG	TGGTAGGCAT	CTCATCTTCT	GCCATTCCAA	GAAAAAATGT	360
GATGAACTCG	CCAAGCAACT	GACCAGCCTG	GGCGTGAACG	CCGTGGCATA	TTATAGAGGT	420
CTAGACGTCG	CCGTCATCCC	CACAGCAGGA	GACGTGGTCG	TGTGCAGCAC	CGACGCGCTC	480
ATGACGGGAT	TCACCGGCGA	CTTTGATTCT	GTCATAGACT	GCAACTCCGC	CGTCACTCAG	540
ACGGTGGACT	TCAGTCTGGA	TCCCACTTTT	ACCATTGAGA	CTACCACAGT	GCCCCAGGAC	600
GCAGTGTCCA	GAAGCCAGCG	TAGGGGCCGC	ACGGGGAGAG	GTAGGCACGG	CATATACCGG	660
	CTGGAGAGAG					720
TACGATGCCG	GATGTGCGTG	GTATGATCTG	ACTECTGEEG	AGACTACCGT	GAGGTTGCGC	780
GCTTACATAA	ACACCCCCGG	GCTCCCTGTC	TGTCAGGACC	ATTTGGAATT	CTGGGAGGG	840
GTGTTCACGG	GGCTCACTÀA	CATCGACGCT	CACATGCTGT	CACAGACCAA	ACAGGGTGGG	900
GAGAATTTNC	CATACCTTGT	AGCGTACCAA	GCAACAGTCT	GTGTTCGCGC	GAAAGCGCCC	960

CCCCCCAGCT	GGGACACAAT	GTGGAAATGC	ATGCTCCGTC	TCAAACCGAC	TTTAACTGGC	1020
CCTACTCCCC	TCTTGTACAG	GCTGGGGCCC	GTCCAGANTG	AGATCACACT	GACGCACCCC	1080
				AGGTCATTAC		1140
GTTCTGGTGG	GGGGCGTTGT	GCCGCCCTG	GCGGCCTACT	GCTTGACGGT	GGGTTCGGTA	1200
GCCATAGTCG	GTAGGATCAT	CCTCTCTGGG	AAACCTGCCA	TCATTCCCGA	TAGGGAGGCA	1260
TTATACCAGC	AATTTGATGA	GATGGAGGAG	TGCTCGGCCT	CSTTGCCCTA	TATGGACGAG	1320
ACACGTGCCA	TTGCCGGACA	ATTCAAAGAG	AAAGTGCTCG	GCTTCATCAG	CACGACCGGC	1360
CAGAAGGCTG	AAACTCTGAA	GCCGGCAGCC	ACGICTGTGT	GGAACAAGGC	TGAGCAGTTC	1440
TGGGCCACAT .	ACATGTGGAA	CTTCATCAGC	GÇGATACAAT	AAŢAG	-	1485

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr 1 5 10 15

Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val 20 25 30

Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35 40 45

Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val

Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro. His Pro 65 70 75 80

Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr

Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile

Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr 115 120 125

Se	130	Gly	/ Val	. Asn	Ala	Val 135	Ala	TYE	Tyr	Arg	Gly 140	Leu	Asp	Val	Ala
Va)	Ile	Pro	Thr	Ala	Gly 150	Asp	Val	Val	Val	Суз 155	Ser	Thr	qzA	Ala	Leu 160
Met	Thr	Gly	Phe	Thr 165	Gly	Asp	Phe	Asp	Ser 170		Ile	Asp	Сув	Asn 175	Ser
Ala	Val	Thr	Gln 180	Thr	Val	qzA	Phe	Ser 185	Leu	Asp	Pro	Thr	Phe 190	Thr	Ile
Glu	Thr	Thr 195	Thr	Val	Pro	Gln	გან 200	Ala	Val	Ser	Arg	Ser 205	Gla	Arg	Arg
Gly	Arg 210	Thr	Gly	Arg	Gly	Arg 215	His	Gly	Ile	īyr	Arg 220	Tyr	Val	Ser	Ala
G1y 225	Glu	λīg	Xaa	Ser	Asp 230	Met	Phe	λsp	Ser	Val 235	Val	Leu	Cys	Glu	Cys 240
Tyr	Asp	λla	Gly	Cys 245	Ala	Trp	Tyr	Asp	Leu 250	Thr	Pro	Ala	Glu	Thr 255	Thr
Val	Arg	Leu	Arg 260	λla	īyī	Ile	λsn	Thr 265	Pro	Gly	Leu	Pro	Val 270	Cys	Gla
Asp	His	Leu 275	Glu	Phe	Įżż	Glu	Gly 280	Val	Phe	Thr	Gly	Leu 285	Thr	Asn	Ile
Ąsp	Ala 290	His	Met	Leu	Ser	Gl= 295	Thr	Lys	Gla	Gly	Gly 300	Glu	Asa	Xaa	Pro
Tyr 305	Leu	Val	Ala	īγΞ	Gln 310	Ala	Thr	Val	Cya	Val 315	Arg	Ala	ŗ'ns	Ala	Pro 320
Pro	Pro	Ser	Trp	Asp 325	Thr	Met	Trp	Lys	Cys 330	Met	Leu	Arg	Leu	Lys 335	Pro
Thr	Leu	Thr	Gly 340	Pro	Thr	Pro	Leu	Leu 345	Tyr	Arg	Leu	Gly	Pro 350	Val	Gln
Xaa	Glu	Ile 355	Thr	Leu	Thr	His	360 250	Ile	Thr	Lys	Tyr	Ile 365	Met	Ala	Cys
Met	Ser 370	Ala	Asp	Leu	Glu	Val 375	Ile	Thr	Xaa	Thr	Trp 380	Val	Leu	Val	Gly
Gly 385	Val	Val	Ala	Ala	Leu 390	Ala	A la	Tyr	Cys	Leu 395	Thr	Val	Gly	Ser	Val 400
Ala	Ile	Val	Gly	Arg 405	Ile	Ile	Leu	Ser	Gly 410	Lys	Pro	Ala	Ile	Ile 415	Pro
Asp	Arg	Glu	Ala 420	Leu	Tyr	Gln	Gln	Phe 425	Asp	Glu	Mec	Glu	Glu 430		Ser
_															

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Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

258

440

638693.081500 PCT/EP94/01323

445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
450 455

Thr Leu Lys Pr Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe 465 470 475 480

Tro Ala Thr Tyr

435

- (2) INFORMATION FOR SEQ ID NO: 201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 2..337
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:
- C TCC ACT GTG ACT GAG AGA GAC ATC AGG GTC GAA GAA GAA GTC TAT 46
 Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr
 1 5 10 15
- CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA ACC GCC CTC

 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu

 20
 25
 30
- ACG GAG AGA CTC TAC GTG GGC GGC CCT ATG TAC AAT AGC AAG GGA GAC

 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp

 40

 45
- CTT TGC GGG TAT CGC AGG TGC CGC GCA AGC GGC GTA TAT ACC ACC AGC
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser
 50 55 60
- TTC GGG AAC ACA CTG ACG TGC TAC CTT AAA GCC TCA GCA GCC ATC AGG
 Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg
 65 70 75
- GCT GCG GGG CTG AAG GAC TGC ACC ATG CTG GTT TGC GGT GAC GAC TTA Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu 80 90 95



GTC GTG ATC GCT GAA AGC GGT GGC GTC GAG GAG GAC AAG CGA GCC CTC 334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu
100 105 110

GGA GCT Gly Ala 340

- (2) INFORMATION FOR SEQ ID NO: 202:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln

1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 203:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(i	٧١	FEATURE :
1-	~ /	PEALURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide.

(B) LCCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

C I	CC A er T	CA G	TG A	CT G	AA A lu A S	GA G	AC A sp I	TC A le A	ऋते ∧	TC G al G 10	AG G	AA G	AG G lu V	al T	AC Y= 15	46
CAG Gln	TGT Cys	TGT Cys	GAC Asp	CTG Leu 20	GAG Glu	bro CCI	GAA Glu	ACC Thr	CGC Arg 25	Lys	GTA Val	ATA Ile	TCT Ser	GCC Ala 30	CTC Leu	94
ACT Thr	GAA Glu	AGA Arg	CTC Leu 35	TAT Tyr	GTG Val	GGC Gly	GGT Gly	CCC Pro 40	ATG Mec	CAC His	AAC Asa	AGC Ser	AGG Arg 45	GGA Gly	GAC Asp	142
CTA Leu	TGC Cys	GGG Gly 50	TAC Tyr	CGT Arg	AGA Azg	TGC Cys	CGC A2g 55	GCG Ala	AGC Ser	GJ y	GTA Val	TAC Tyr 60	ACC Thr	ACA Thr	AGC Ser	· 190
TTC Phe	GGG Gly 65	AAC Asn	ACT Thr	CTG Leu	ACG Thr	TGC Cys 70	TTC Phe	CTC Leu	Aag Lys	GCC Ala	ACA Thr 75	GCG Ala	GCC Ala	ACC Thr	AAA Lys	238
GCC Ala 80	GCT Ala	GGC Gly	CTA Leu	aag Lys	GAC Asp 85	TGC Cys	ACC Thr	ATG Met	TIG Leu	GTG Val 90	TGT Cys	GGT Gly	GAC Asp	GAC Asp	TTA Leu 95	286
GTC Val	GTT Val	ATC Ile	GCC Ala	GAA Glu 100	AGC Ser	GAT Asp	GGT Gly	GTC Val	GAA Glu 105	GAG Glu	GAC Asp) CGC	Arg Arg	GCC Ala 110	CTC Leu	334
GGA Gly																340

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

142

Cys	Сув	Asp	Leu 20	Glu	Pro	Glu	Thr	Ar g 25	Lys	Val	Ile	Ser	Ala 30	Leu	Thr		
Glu	Arg	Leu 35	Tyr	Val	Gly	Gly	Pro 40	Met	His	Asd	Ser	Arg 45	Gly	qzA	Leu		
Суз	Gly 50	:yr	Arg	بن	Cys	Arg 55	λla	Ser	Gly	Val	Ty: 60	Thr	Thr	Ser	⊋he		
Gly 65	Asn	Thr	Leu	Thr	Cys 70	Phe	Leu	Lys	Ala	Thr 75	Ala	Ala	Thr	Lys	Ala 80		
Ala	Gly	Leu	Lys	Asp 85	Cys	Thr	Met	Leu	Val 90	Суз	Gly	qeA	Asp	Leu 95	Val		
Val	Ile	Ala	Glu 100	Ser	Asp	Gly	Val	Glu 105		Asp	Arg	Arg	Ala 110	Leu	Gly	-	
Ala																	
(2)	INF	ORMA:	TION	FOR	SEQ	ID 1	NO: 1	205 :									
	(1)		QUENC A) Li						a								•
			B) I					-	3								
		•	c) s:					_						-			
		(1	D) TO	OPOL	OGY:	lin	ear										
	(11) MO	LECU	LE T	YPE:	cDN.	λ										
	(111) HY	POTH	ETIC	AL:	NO										·	
	(iii) AN	TI-S	ENSE	: NO												
	(ix) FE	ATUR:	Ξ:													
		(.	A) N	AME/	KEY:	CDS											
		C	B) L	OCAT	ION:	2	340										
	11+) EE	ATUR	- .											•		
	,		A) N		KEY:	mat	pep	tide	!								
			B) L														
	(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	10: 2	05:						
			TG A														46
S		hr V	al T	hr G	_	rg A	sp I	le A	urg I		lu G	lu (lu 1	lle 7	lyr 15		
	1				5					10					13		
															CTA		94
Gln	Çys	Cys	Asp	Leu 20		Pro	Glu	Ala	Arg 29	-	: Val	. Ile	e Se	2 Ala 30	Leu	•	
															-		

ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC

Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp 35 40 45

CTA Leu	CÀZ	GGG Gly 50	CAA Gln	CGG Arg	AGG Arg	TGC Cys	CGC Arg 55	GCA Ala	AGC Ser	GGG Gly	GTC Val	TAC Tyr 60	ACC Thr	ACC Thr	AGC Ser		190
TTC Phe	65 GCG	AAC Asn	ACT Thr	GTA Val	ACG Thr	TGT Cys 70	TAT Tyr	CTC Leu	AAG Lys	GCC Ala	G.T Val 75	GC3 Ala	GCT Ala	ACT Thr	AGG Arg		238
GCC Ala 80	GCA Ala	GCT Gly	CTG Leu	aaa Lys	GGT Gly 85	TGC Cys	AGC Ser	ATG Met	CTG Leu	GTT Val 90	cie Cie	GGA Gly	GAC Asp	gac	TTA Leu 95		286
GTC Val	GTC Val	ATC Ile	TGC Cys	GAG Glu 100	AGC Ser	ej ^a eec	GGC Gly	GTA Val	GAG Glu 105	GAG Glu	gat Asp	GCA Ala	AGA Arg	GCC Ala 110	CTC Leu		334
CGA Arg																•	340

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

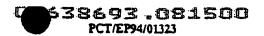
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala 65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 207:



(i)	SECUENCE	CHARACTERISTICS:
-----	----------	------------------

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

		G GTC GAG GAA GAC g Val Glu Glu Glu 10	· 46
		CGC AAG GTG ATA 1 Arg Lys Val Ile 8 25	94
		ATG TAT AAC AGC I Met Tyr Asn Ser I	142
		AGC GGG GTA TAC A Ser Gly Val Tyr :	190
		ANA GCC ACA GCA (Lys Ala Thr Ala) 75	238
		CTG GTA TGC GGT (Leu Val Cys Gly 2	286
		GAG GAG GAC GCC (Glu Glu Asp Ala (105	334
CGA GCC			340

(2) INFORMATION FOR SEQ ID NO: 208:

Arg Ala

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208: Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln

1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr

Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala 65 70 75 60

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg

Ala

- (2) INFORMATION FOR SEQ ID NO: 209:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..340
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

CCCCACCGTG ACNGAGAGGG ACNTCAGGGT CGAGGAAGAG GTCTATCAGT GCTGTAATCT

60

GGAGNCCGAT GNCCGCAAGG TCATCAACGC CCTCACAGAG AGACTCTACG TGGGCGGCCC

120

TATGCACAAC	AGCAAGGGAG	ACCTGTGTGG	CATCOGTAGA	TGCCGCGCGA	GCGGCGTTTA	180
CACCACGAGC	TTCGGAAACA	CGCTGACTTG	CTACCTCAAA	GCCACAGCGG	CCACCAGGGC	240
CGCGGGCTTG	AAGGATTGCA	CCATGCTGGT	CTGCGGRIGAC	GACCTGGTTG	TCATTGCTGA	300
GAGCATTGGC	ATAGACGASG	ACAAGCAAGC	CCTCCGGRCT			340

- (2) INFORMATION FOR SEQ ID NO: 210:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Pro Thr Val Thr Glu Arg Asp Xaa Arg Val Glu Glu Glu Val Tyr Glm

Cys Cys Asn Leu Glu Xaa Asp Xaa Arg Lys Val Ile Asn Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Ile Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 60

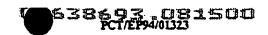
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala 65 70 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Ile Gly Ile Asp Glu Asp Lys Gln Ala Leu Arg 100 105 110

Thr

- (2) INFORMATION FOR SEQ ID NO: 211:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA



(111)	HYPOTHETICAL.	370
	MARGINE ILAI.	MI 3

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/REY: CES
(B) LOCATION: 1.:340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

C	TCGACTGTG	NCCGAGAGGG	ACATCAGGAC	AGAGGGAGAG	GTCTATCAGT	GTTGCGACCT	60
G	gaaccggaa	GCCCGCAAGG	TAATCACCGC	CCTCACTGAG	AGACTCTATG	TGGGCGGACC	120
C	ATGTTCAAC	AGCAAGGGAG	ACCTGTGCGG	ACAACGCCGG	TGCCGCGCAA	GCGGCGTGTT	180
C	ACCACCAGC	TTCGGGAACA	CACTGACGTG	CTACCTTAAA	GCCACAGCTG	CTACTAGAGC	240
A	GCCGGCTTA	AAAGATTGCA	CCATGCTGGT	CTGCGGTGAC	GACTTAGTCG	TTATTTCCGA	300
G	AGCGCCGGT	GTGGAGGAGG	ATCECANAAC	COINCEACOI			340

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Ser Thr Val Xaa Glu Arg Asp Ile Arg Thr Glu Gly Glu Val Tyr Gln 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Phe 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala

267

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85

Val Ile Ser Glu Ser Ala Gly Val Glu Glu Asp Pro Xaa Thr Xaa Arg 100

Pro

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 2..340
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..337
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:
- C TCA ACA GTC ACC GAG AAC GAC ATC CGT GTT GAG GAG TCA ATT TAC 45 Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr 1 5 15 CAA TOT TGT GAC TTG GCC CCC GAG GCC AGA CAG GCC ATA AAG TCG CTC 94 Gin Cys Cys Asp Leu Ala Pro Glu Ala Arg Gin Ala Ile Lys Ser Leu 20 ACA GAG CGG CTT TAT ATC GGG GGT CCC CTG ACT AAT TCA AAG GGG CAG 142 Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln 35 45 AAC TGT GGC TAT CGC CGA TGC CGC GCA AGC GGC GTG CTG ACG ACC AGC Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser 50 TGC GGT AAT ACC CTT ACA TGT TAC"CTA ANG GCC TCT GCA GCC TGT CGA 238 Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg 65 70

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GCT GCG AAG CTC CAG GAC TGC ACG ATG CTC GTG TGC GGG GAC GAC CTT

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95

CGA GTC
Arg Val

- (2) INFORMATION FOR SEQ ID NO: 214:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Gla Ala Ile Lys Ser Leu Thr 20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn 35

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala 65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg 100 105 110

Val

- (2) INFORMATION FOR SEQ ID NO: 215:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CONA

(iii)	HYPOTHETICAL:	NO
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(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

C TCA AC Ser Th	C GTC AG	CG GAG AG ar Glu Ar	G GAT AT g Asp Il	e Arg Th	EA GAA GE EF Glu GI LO	A TCC A1 lu Ser II	TA TAT Le Tyr 15	- 46
CAA GCT	TGT TCC	CTG CCC	CAA GAG	GCC AGA	ACT GTC	ATA CÁC	TCG CTC	94
GIN ALA	Cys Ser	Leu Pro	Gin Glu	Ala Arg 25	Thr Val	Ile His	Ser Leu 30	
ACC GAG	AGA CTC	TAC GTG	GGA GGG	CCC ATG	ATA AAC	AGC AAA	GGG CAA	142
Thr Glu	Arg Leu 35	Tyr Val	Gly Gly	Pro Mes 40	Ile Asn	Ser Lys	Gly Glm	·
TCC TGC	GGT TAC	AGG CGT	TGC CGC	GCA AGC	GGT GTT	TTC ACC	ACC AGC	190
Ser Cys		Arg Arg		Ala Ser	Gly Val		Thr Ser	
	50		55			60		
ATG GGG	AAT ACC	ATG ACG	TGT TAC	ATC AAA	GCC CTT	GCA GCG	TGT AAA	238
Met Gly .	Asn Thr	Met Thr	Cys Tyr 70	Ile Lys	Ala Leu 75	Ala Ala	Cys Lys	
GCC GCA	GGG ATC	GTG GAC	CCC GTC	ATG CTG	GTG TGT	GGA GAC	GAC CTG	286
Ala Ala	Gly Ile	Val Asp	Pro Val	Met Leu	Val Cys	Gly Asp	Asp Leu	
80		85			90		95	
GTC GTC	ATC TCG	GAG AGC	CAG GGT	AAC GAG	GAG GAC	GAG CGA	AAC CTG	334
Val Val	Ile Ser	Glu Ser	Gln Gly		Glu Asp	Glu Arg		
		100		105			110	
AGA GCT								340
Arg Ala								

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln 1 5 10 15

Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met 50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala 65 70 75 80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NC: 217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid -
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 2..340
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:
- C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr 1 5 10 15
- CAA TGC TGC AAC CTT GAA CCG GAG GCC AGG AAA GTG ATC TCC CTC Gln Cys Cys Asn Leu Glu Pro Giu Ala Arg Lys Val Ile Ser Ser Leu

	•		20			25			30			
							AAC Asn				٠	142
		TAT			GCC		GTT Val	CCI				190
							ACA The 75					238
							TGC Cys			-		286
					Va.		GAT Asp				•	334
AGA												340

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERÍSTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1 5 10 15

Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr 20 25 30

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala 65 ' 70 75 80

Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 219:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 220:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 221:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Arg Thr Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 222:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 629 base pairs

(B)	TYPE: nucleic	acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY: lin	ear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

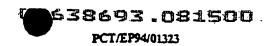
(A) NAME/KEY: CDS
(B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

	,,	•						-								
						STC T								sp À	la	47
	1				5					10					15	
						AAG Lys										95
						GTG Val										143
AGT Ser	TGG Trp	GAC Asp 50	Glu	ATG Met	TGG Trp	AAG Lys	TGT Cys 55	CTC Leu	GTA Val	CGG Arg	CTT Leu	AAG Lys 60	CCA Pro	ACA Thy	CTA Leu	191
CAT His	GGA Gly 65	CCT	ACG Thr	Pro	CTT Leu	CTA Leu 70	TAT Tyr	CGG Arg	TTG Leu	gly GGG	CCT Pro 75	GTC Val	CAA Gln	aat Asn	G}n GYY	239
ATC Ile 80	TGC Cys	TTG	ACA Thr	CAC	85 85	ATC	ACA Thr	AAA Lys	TAC Tyr	ATC Ile 90	ATG Met	GCA Ala	TGC Cys	ATG Met	TCA Ser 95	287
GCT Ala	GAT Asp	CTG	GAA Glu	GTA Val	The	ACC Thr	AGC Ser	ACC The	TGG Trp 105	Val	TTG	CTT	GGA	GGG Gly 110	GTC Val	335
CTC Leu	GCG Ala	GCC	CTA Leu 115	Ala	GCC Ala	TAC Tyr	TGC Cys	120	: Ser	GTC Val	GLY	TGT Cys	GTT Val 125	Val	ATT	383
GTG Val	GGT Gly	CAT His	Ile	GAC	CTC	GGG Gly	GGC Gly 139	/ Lys	CCG	GCA Ala	ATC	GTT Val	Pro	GAC Qea	Lys	431



GAG Glu	GTG Val 145	Leu	TAT Tyr	GT¤ CYY	CAA Gln	TAC Ty= 150	GAT Asp	GAG Glu	ATG Net	GAA Glu	GAG Glu 155	Cys Cys	TCA Ser	CAA Gln	GCT Ala	479
GCC Ala 160	CCA Pro	TAT Tyr	ATC Ile	GAA Glu	CAA Gl:: 165	GCT Ala	CAG Gln	GTA Val	ATA Ile	GCT Ala 170	CAC His	CAG Gln	TTC Phe	AAG Lys	GAA Glu 175	\$27
Lys	GTC Val	CTT Leu	GGA Gly	TTG Leu 180	CTG Leu	CAG Gln	CGA	GCC Ala	ACC Thr 185	CAA Glm	CAA Gln	CAA Gln	GCT Ala	GTC Val 190	ATT Ile	\$75
GAG Glu	CCC Pro	ATA Ile	GTA Val 195	ACT Thr	ACC Thr	aac Asii	TGG Trp	CAA Gln 200	aag Lys	CTT Leu	GAG Glu	GCC Ala	TTT Phe 205	Izp IGG	CAC His	623
AAG Lys																629 -

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 1 5 10 15

Phe Leu Ser Gin Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr 20 25 30

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His 50 55 60

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 65 70 75 80

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 85 90 95

Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu
100 105 110

Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val

Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu 130 135 140



Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala 145 150 155 160

Pr Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys 165 170 175

Val Leu Gly Leu Leu Gin Arg Ala Thr Gln Gln Gln Ala Val Ile Glu 180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys
195 200 205

His

- (2) INFORMATION FOR SEQ ID NO: 224:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 2..12
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

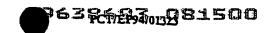
Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile

1 5 10

- (2) INFORMATION FOR SEQ ID NO: 225:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - . (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:
 - Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:
- Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile
- (2) INFORMATION FOR SEQ ID NO: 227:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amine acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:
 - Val Asm Tyr His Asm Thr Ser Gly Ile Tyr His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 228:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:
 - Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 229:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val

1 10

- (2) INFORMATION FOR SEQ ID NO: 232:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amine acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val 1 5 10

(2) INFORMATION FOR SEQ ID NO: 233:



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MCLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:
- Val Tyr Glu Ala Asp Tyr His Ile Leu His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 234:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:
 - Val Tyr Glu Thr Asp Asn His Ile Leu His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 235:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTE: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:
 - Val Tyr Glu Thr Glu Asn His Ile Leu His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 236:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 237:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

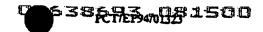
Val Phe Glu Thr Glu His His Ile Leu His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 238:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 239:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu 1 5 10



- (2) INFORMATION FOR SEQ ID NO: 240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 241:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gin Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 242:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242: Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 243:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 244:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amine acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: pertide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asm Glm Ser Arg Cys Trp Val Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 245:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amine acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:
 - Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu

1 5 10

- (2) INFORMATION FOR SEQ ID NO: 247:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val Lys Thr Gly Asn Ser Val Arg Cys Trp Ile Pro Leu
1 5 10

- (2) INFORMATION FOR SEQ ID NG: 248:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val Lys Thr Gly Asm Val Ser Arg Cys Trp Ile Ser Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NG: 249:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val Arg Lys Asp Asm Val Ser Arg Cys Trp Val Glm Ile
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 250:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 251:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTE: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 252:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252;

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 253:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:



Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 254:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 255:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 256:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLZCULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro 1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

, ,

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 258:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 259:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (3) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 260:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pr Leu Thr Ser
1 S 10

- (2) INFORMATION FOR SEQ ID NO: 251:
 - (i) SEQUENCE CHARACTERISTICS:
 - . (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULZ TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 252:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 263:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids.
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp 1 5

(2) INFORMATION FOR SEQ ID NO: 254:



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser Pro Gln His His Lys Phe Val Gln Asp 1 5 10

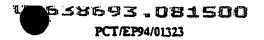
- (2) INFORMATION FOR SEQ ID NO: 265:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Arg Pro Arg Arg Leu Trp Thr Thr Gln Glu
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 266:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Pro Pro Arg Ile His Glu Thr Thr Gln Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 267:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 268:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - ' (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gin Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser

. Trp Ala Gln

- (2) INFORMATION FOR SEQ ID NO: 269:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1443
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..1443
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC

Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

289

									-							
1				5					10					15		
CTT	GCT	GAT	GGA	GGG	TGT	TCA	GGC	ccc	ece	TAT	GAC	GTG	እተ <u></u>	277	~	
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Val	Ile	Ile	CAR	96
			20				•	25		•	•		30		-,-	
C) C	C3.C	***	~>~	800	636	~>~										
Ass	Glu	100	His	Ser	CAG Glm	LEAL	GCC A:a	ACC	ACC	ATT	CIT	GGG	ATA	GGC	ACT	144
	-	35				,	40	****	****		nea	45	8	Giğ	inr	
GTC Val	CIT	GAC	CAG	GCA	GAG Glu	ACG	GCT	GGA	GCT	AGG	CIC	GIC	GTC	TTG	GCC	192
***	50	بوجہ	9211	AL a	GIG	55	AL a	GTÅ	ALG	wid	Leu 60	va÷	vaı	Leu	Aia	
											-					
ACG	GCC	ACC	CCT	CCC	GGC	AGT	GTG	ACA	ACG	CCC	CAC	CCC	AAC	ATC	GAG	240
65	WTS	TAY	PIO	PIO	Gly 70	Ser	Val	Thr	Thr	P20	His	510	Asn	Ile		
•••										/3					80	_
GAA	GTG	GCC	CTG	CCT	CAG	GAG	GGG	gag	GTT	CCC	TTC	TAC	GGC	AGA	GCC	288
Glu	Val	Ala	Leu		Gln	Glu	Gly	Glu		Pro	Phe	Tyr	Gly	-	Ala	
				85					90					95		
ATT	CCC	CIT	GCT	TTT	ATA	AAG	GGT	GGT	AGG	CAT	CTC	ATC	TTC	TGC	CAT	336
Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	
			100					105					110			
TCC	AAG	AAA	AAA	TGT	GAT	GAA	cic	GCC	AAG	CAA	CTG	ACC	AGC	CTG	GGC	384
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr	Ser	Leu.	Gly	
		115					120					125				
GTG	AAC	GCC	GTG	GCA	TAT	TAT	AGA	GGT	دجم	GAC	GTC	GCC	GTC	A ===	CCC	432
Val	Asn	Aia	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ala	Val	Ile	Pro	
	130					135					140					
ACA	GCA	GGA	GAC	GTG	GTC	GTG	TGC	AGC	ACC	GSC	ece	مبنت	e TG	n.cc	CCD	480
Thr	Ala	Gly	qzA	Val	Val	Val	Cys	Ser	Thr	Asp	Ala	Leu	Mec	Thr	Gly	450
145					150					155					160	
TTC	ACC.	car	GBC	بتحوي	CAT	т Ст	CTC	277	636	***						
Phe	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cvs	AAC	Ser	Ala	Val	Thr	528
		Ū	-	165	•				170					175		
CAC	».cc		C3.C			-	~`									
Gln					AGT Ser											576
			180					185		•			190	• • • •	****	
ACA Thr																624
		195		no p	724	461	200	~~	361	GIII	ALG	205	Gry	Arg	Int	
GGG	AGA	GGT	AGG	CAC	GGC	ATA	TAC	CGG	TAT	GTC	TCG	GCT	GGA	GAG	AGA	672
Gly	210	atà	nig	uT2	GTÅ	215	TAI	wij	IAL	AT	Ser 220	ALA	стÅ	GIU	AIG	
							•									
CCG	TCT	GAC	ATG	TTC	GAC	TCC	GTG	GTG	CTC	TGT	GAG	TGC	TAC	GAT	GCC	720
Pro 225	ser	Asp	met	Pne	230	ser	val	va!	Leu	Cys 235	Glu	СЛа	Tyr	Asp	Ala 240	
															- 40	

GGA Gly	TGT Cys	GCG	TGG	TAT Tyr 245	GAT Asp	CTG Leu	ACT Thr	CCT Pro	GCC Ala 250	GAG Glu	ACT Thr	ACC	GTG Val	AGG Arg 255	TTG Leu	768
CGC	GCT Ala	TAC	ATA Ile 260	AAC Asn	ACC Thr	Pro	GGG Gly	CTC Leu 265	S.c.	GTC Val	càr ICI	CAG Gln	GAC Asp 270	CAT His	TTG Leu	816
Glu	Phe	Trp 275	Glu	Gly	GTG Val	Phe	Thr 280	Gly	Leu	The	Asn	Ile 285	Asp	Ala	His	864
Met	Leu 290	Ser	Gla	Thr	aaa Lys	Gln 295	G ₂ y	G1A	Glu	Asa	7he 300	510	īy:	Leu	Val	912
Ala 305	Tyr	Gln	Ala	Thr	GTC Val 310 AAA	Суѕ	Val	yzd	λia	Lys	Ala	Pro	Pro	Pro	Ser 320	960
Irp	Asp	Thr	Met	Trp 325	Lys	Cys	Mec	Leu	Arg 330	Leu	Lys	Pro	Thr	Leu 335	Thr	1008
Gly	5.0	Thr	PT0 340	Leu	TTG Leu	ī'nī	Arg	Leu 345	Gly	710	Val	Glm	Asn 350	Glu	Ile	1056
ACA Thr	CTG Leu	ACG Thr 355	CAC His	CCC	ATC Ile	ACC Thr	AAG Lys	TAC	ATT Ile	ATG Met	GCT Ala	TGC Cys 363	ATG Met	TCT Ser	GCG Ala	1104
qzA	TTG Leu 370	GAG Glu	GTC Val	ATT Ile	ACC Thr	AGC Ser 375	ACT Thr	TGG Tæp	GTT Val	CTG Leu	GTG Val 330	GJÀ	GGC Gly	GTT Val	GTG Val	1152
GCG Ala 385	GCC Ala	CTG Leu	GCG Ala	GCC Ala	TAC Tyr 390	TGC Cys	TTG Leu	ACG Thr	GTG Val	GGT Gly 395	TCG Ser	GTA Val	GCC Ala	ATA Ile	GTC Val 400	1200
GGT Gly	AGG Arg	ATC Ile	ATC Ile	CTC Leu 405	TCT Ser	GGG	AAA Lys	Pro	GCC Ala 410	ATC Ile	ATT Ile	Pro	gat Asp	AGG Arg 415	GAG Glu	1249
GCA Ala	TTA Leu	TAC Tyr	CAG Gln 420	Gln	TTT Phe	GAT Asp	GAG Glu	ATG Met 425	GAG Glu	GAG Glu	TGC Cys	TCG Ser	GCC Ala 430	TCG Ser	TTG Leu	1296
	Tyr				ACA Thr											1344
Val					AGC Ser											1392
Pro .	GCA Ala	GCC Ala	ACG Thr	TCT Ser	GTG Val 470	TGG Trp	AAC Asn	AAG Lys	GCT Ala	GAG Glu 475	CAG Gln	TTC Phe	TGG Trp	GCC Ala	ACA Thr 480	1440

TAC Tyr

1443

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NG: 270:

Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe
1 5 10 15

Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys
20 25 30

Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr
35 40 45

Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 50 60

Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asm Ile Glu 65 70 75 80 Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala

Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His

Ser Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly 115 120 125

Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro 130 135 140

Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly
145 150 155 160

Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 180 195 190

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr
195 200 205

Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg 210 215 220

Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala

292

225 230 235 Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu 245 250 Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 260 265 Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Glu Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 345 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val 375 Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys 455 Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr 470

Tyr